(19) Europäisches Patentamt
European Patent Office
Office européen des brevets

(11) EP 1 108 790 A2

(12) EUROPEAN PATENT APPLICATION

(43) Date of publication:
20.06.2001 Bulletin 2001/25

(21) Application number: **00127688.0**

(22) Date of filing: **18.12.2000**

(51) Int Cl.7: **C12Q 1/68**, C07H 21/04, C12N 15/63, C07K 14/34, C12R 1/15, G06F 17/00, C12R 1/13, G01N 33/50

(84) Designated Contracting States:
AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE TR
Designated Extension States:
AL LT LV MK RO SI

(30) Priority: **16.12.1999 JP 37748499**
07.04.2000 JP 2000159162
03.08.2000 JP 2000280988

(83) **Declaration under Rule 28(4) EPC (expert solution)**

(71) Applicant: **KYOWA HAKKO KOGYO CO., LTD.**
Chiyoda-ku, Tokyo 100-8185 (JP)

(72) Inventors:
- **Nakagawa, Satochi,**
  c/o Kyowa Hakko Kogyo Co.,Ltd.
  Machida-shi, Tokyo 194-8533 (JP)
- **Mizoguchi, Hiroshi,**
  c/o Kyowa Hakko Kogyo Co.,Ltd.
  Machida-shi, Tokyo 194-8533 (JP)
- **Ando, Seiko, c/o Kyowa Hakko Kogyo Co., Ltd.**
  Machida-shi, Tokyo 194-8533 (JP)
- **Hayashi, Mikiro,**
  c/o Kyowa Hakko Kogyo Co.,Ltd.
  Machida-shi, Tokyo 194-8533 (JP)
- **Ochiai, Keiko, c/o Kyowa Hakko Kogyo Co.,Ltd.**
  Machida-shi, Tokyo 194-8533 (JP)
- **Yokoi, Haruhiko,**
  c/o Kyowa Hakko Kogyo Co.,Ltd.
  Machida-shi, Tokyo 194-8533 (JP)
- **Tateishi, Naoko,**
  c/o Kyowa Hakko Kogyo Co.,Ltd.
  Machida-shi, Tokyo 194-8533 (JP)
- **Senoh, Akihiro, c/o Kyowa Hakko Kogyo Co.,Ltd.**
  Machida-shi, Tokyo 194-8533 (JP)
- **Ikeda, Masato, c/o Kyowa Hakko Kogyo Co.,Ltd.**
  Machida-shi, Tokyo 194-8533 (JP)
- **Ozaki, Akio, c/o Kyowa Hakko Kogyo Co., Ltd.**
  Hofu-shi, Yamaguchi 747-8522 (JP)

(74) Representative: **VOSSIUS & PARTNER**
Siebertstrasse 4
81675 München (DE)

(54) Novel polynucleotides

(57) Novel polynucleotides derived from microorganisms belonging to coryneform bacteria and fragments thereof, polypeptides encoded by the polynucleotides and fragments thereof, polynucleotide arrays comprising the polynucleotides and fragments thereof, recording media in which the nucleotide sequences of the polynucleotide and fragments thereof have been recorded which are readable in a computer, and use of them.

EP 1 108 790 A2

Description

BACKGROUND OF THE INVENTION

1. Field of the Invention

[0001] The present invention relates to novel polynucleotides derived from microorganisms belonging to coryneform bacteria and fragments thereof, polypeptides encoded by the polynucleotides and fragments thereof, polynucleotide arrays comprising the polynucleotides and fragments thereof, computer readable recording media in which the nucleotide sequences of the polynucleotide and fragments thereof have been recorded, and use of them as well as a method of using the polynucleotide and/or polypeptide sequence information to make comparisons.

2. Brief Description of the Background Art

[0002] Coryneform bacteria are used in producing various useful substances, such as amino acids, nucleic acids, vitamins, saccharides (for example, ribulose), organic acids (for example, pyruvic acid), and analogues of the above-described substances (for example, N-acetylamino acids) and are very useful microorganisms industrially. Many mutants thereof are known.

[0003] For example, *Corynebacterium glutamicum* is a Gram-positive bacterium identified as a glutamic acid-producing bacterium, and many amino acids are produced by mutants thereof. For example, 1,000,000 ton/year of L-glutamic acid which is useful as a seasoning for umami (delicious taste), 250,000 ton/year of L-lysine which is a valuable additive for livestock feeds and the like, and several hundred ton/year or more of other amino acids, such as L-arginine, L-proline, L-glutamine, L-tryptophan, and the like, have been produced in the world (*Nikkei Bio Yearbook 99*, published by Nikkei BP (1998)).

[0004] The production of amino acids by *Corynebacterium glutamicum* is mainly carried out by its mutants (metabolic mutants) which have a mutated metabolic pathway and regulatory systems. In general, an organism is provided with various metabolic regulatory systems so as not to produce more amino acids than it needs. In the biosynthesis of L-lysine, for example, a microorganism belonging to the genus *Corynebacterium* is under such regulation as preventing the excessive production by concerted inhibition by lysine and threonine against the activity of a biosynthesis enzyme common to lysine, threonine and methionine, i.e., an aspartokinase, (*J. Biochem., 65*: 849-859 (1969)). The biosynthesis of arginine is controlled by repressing the expression of its biosynthesis gene by arginine so as not to biosynthesize an excessive amount of arginine (*Microbiology, 142*: 99-108 (1996)). It is considered that these metabolic regulatory mechanisms are deregulated in amino acid-producing mutants. Similarly, the metabolic regulation is deregulated in mutants producing nucleic acids, vitamins, saccharides, organic acids and analogues of the above-described substances so as to improve the productivity of the objective product.

[0005] However, accumulation of basic genetic, biochemical and molecular biological data on coryneform bacteria is insufficient in comparison with *Escherichia coli, Bacillus subtilis*, and the like. Also, few findings have been obtained on mutated genes in amino acid-producing mutants. Thus, there are various mechanisms, which are still unknown, of regulating the growth and metabolism of these microorganisms.

[0006] A chromosomal physical map of *Corynebacterium glutamicum* ATCC 13032 is reported and it is known that its genome size is about 3,100 kb (*Mol. Gen. Genet., 252*: 255-265 (1996)). Calculating on the basis of the usual gene density of bacteria, it is presumed that about 3,000 genes are present in this genome of about 3,100 kb. However, only about 100 genes mainly concerning amino acid biosynthesis genes are known in *Corynebacterium glutamicum*, and the nucleotide sequences of most genes have not been clarified hitherto.

[0007] In recent years, the full nucleotide sequence of the genomes of several microorganisms, such as *Escherichia coli, Mycobacterium tuberculosis*, yeast, and the like, have been determined (*Science, 277*: 1453-62 (1997); *Nature, 393*: 537-544 (1998); *Nature, 387*: 5-105 (1997)). Based on the thus determined full nucleotide sequences, assumption of gene regions and prediction of their function by comparison with the nucleotide sequences of known genes have been carried out. Thus, the functions of a great number of genes have been presumed, without genetic, biochemical or molecular biological experiments.

[0008] In recent years, moreover, techniques for monitoring expression levels of a great number of genes simultaneously or detecting mutations, using DNA chips, DNA arrays or the like in which a partial nucleic acid fragment of a gene or a partial nucleic acid fragment in genomic DNA other than a gene is fixed to a solid support, have been developed. The techniques contribute to the analysis of microorganisms, such as yeasts, *Mycobacterium tuberculosis, Mycobacterium bovis* used in BCG vaccines, and the like (*Science, 278*: 680-686 (1997); *Proc. Natl. Acad. Sci. USA, 96*: 12833-38 (1999); *Science, 284*: 1520-23 (1999)).

SUMMARY OF THE INVENTION

[0009] An object of the present invention is to provide a polynucleotide and a polypeptide derived from a microorganism of coryneform bacteria which are industrially useful, sequence information of the polynucleotide and the polypeptide, a method for analyzing the microorganism, an apparatus and a system for use in the analysis, and a method for breeding the microorganism.

[0010] The present invention provides a polynucleotide and an oligonucleotide derived from a microorganism belonging to coryneform bacteria, oligonucleotide arrays to which the polynucleotides and the oligonucleotides are fixed, a polypeptide encoded by the polynucleotide, an antibody which recognizes the polypeptide, polypeptide arrays to which the polypeptides or the antibodies are fixed, a computer readable recording medium in which the nucleotide sequences of the polynucleotide and the oligonucleotide and the amino acid sequence of the polypeptide have been recorded, and a system based on the computer using the recording medium as well as a method of using the polynucleotide and/or polypeptide sequence information to make comparisons.

BRIEF DESCRIPTION OF THE DRAWING

[0011] Fig. 1 is a map showing the positions of typical genes on the genome of *Corynebacterium glutamicum* ATCC 13032.

[0012] Fig. 2 is electrophoresis showing the results of proteome analyses using proteins derived from (A) *Corynebacterium glutamicum* ATCC 13032, (B) FERM BP-7134, and (C) FERM BP-158.

[0013] Fig. 3 is a flow chart of an example of a system using the computer readable media according to the present invention.

[0014] Fig. 4 is a flow chart of an example of a system using the computer readable media according to the present invention.

DETAILED DESCRIPTION OF THE INVENTION

[0015] This application is based on Japanese applications No. Hei. 11-377484 filed on December 16, 1999 No. 2000-159162 filed on April 7, 2000 and No. 2000-280988 filed on August 3, 2000, the entire contents of which are incorporated hereinto by reference.

[0016] From the viewpoint that the determination of the full nucleotide sequence of *Corynebacterium glutamicum* would make it possible to specify gene regions which had not been previously identified, to determine the function of an unknown gene derived from the microorganism through comparison with nucleotide sequences of known genes and amino acid sequences of known genes, and to obtain a useful mutant based on the presumption of the metabolic regulatory mechanism of a useful product by the microorganism, the inventors conducted intensive studies and, as a result, found that the complete genome sequence of *Corynebacterium glutamicum* can be determined by applying the whole genome shotgun method.

[0017] Specifically, the present invention relates to the following (1) to (65):

(1) A method for at least one of the following:

(A) identifying a mutation point of a gene derived from a mutant of a coryneform bacterium.
(B) measuring an expression amount of a gene derived from a coryneform bacterium.
(C) analyzing an expression profile of a gene derived from a coryneform bacterium.
(D) analyzing expression patterns of genes derived from a coryneform bacterium, or
(E) identifying a gene homologous to a gene derived from a coryneform bacterium,
said method comprising:

(a) producing a polynucleotide array by adhering to a solid support at least two polynucleotides selected from the group consisting of first polynucleotides comprising the nucleotide sequence represented by any one of SEQ ID NOS:1 to 3501, second polynucleotides which hybridize with the first polynucleotides under stringent conditions, and third polynucleotides comprising a sequence of 10 to 200 continuous bases of the first or second polynucleotides.
(b) incubating the polynucleotide array with at least one of a labeled polynucleotide derived from a coryneform bacterium, a labeled polynucleotide derived from a mutant of the coryneform bacterium or a labeled polynucleotide to be examined, under hybridization conditions.
(c) detecting any hybridization, and
(d) analyzing the result of the hybridization.

As used herein, for example, the at least two polynucleotides can be at least two of the first polynucleotides, at least two of the second polynucleotides, at least two of the third polynucleotides, or at least two of the first, second and third polynucleotides.

(2) The method according to (1), wherein the coryneform bacterium is a microorganism belonging to the genus *Corynebacterium*, the genus *Brevibacterium*, or the genus *Microbacterium*.
(3) The method according to (2), wherein the microorganism belonging to the genus *Corynebacterium* is selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium callunae*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, and *Corynebacterium ammoniagenes*.
(4) The method according to (1), wherein the polynucleotide derived from a coryneform bacterium, the polynucleotide derived from a mutant of the coryneform bacterium or the polynucleotide to be examined is a gene relating to the biosynthesis of at least one compound selected from an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid, and analogues thereof.
(5) The method according to (1), wherein the polynucleotide to be examined is derived from *Escherichia coli*.
(6) A polynucleotide array, comprising:

at least two polynucleotides selected from the group consisting of first polynucleotides comprising the nucleotide sequence represented by any one of SEQ ID NOS:1 to 3501, second polynucleotides which hybridize with the first polynucleotides under stringent conditions, and third polynucleotides comprising 10 to 200 continuous bases of the first or second polynucleotides, and
a solid support adhered thereto.

As used herein, for example, the at least two polynucleotides can be at least two of the first polynucleotides, at least two of the second polynucleotides, at least two of the third polynucleotides, or at least two of the first, second and third polynucleotides.
(7) A polynucleotide comprising the nucleotide sequence represented by SEQ ID NO:1 or a polynucleotide having a homology of at least 80% with the polynucleotide.
(8) A polynucleotide comprising any one of the nucleotide sequences represented by SEQ ID NOS:2 to 3431, or a polynucleotide which hybridizes with the polynucleotide under stringent conditions.
(9) A polynucleotide encoding a polypeptide having any one of the amino acid sequences represented by SEQ ID NOS:3502 to 6931, or a polynucleotide which hybridizes therewith under stringent conditions.
(10) A polynucleotide which is present in the 5' upstream or 3' downstream of a polynucleotide comprising the nucleotide sequence of any one of SEQ ID NOS:2 to 3431 in a whole polynucleotide comprising the nucleotide sequence represented by SEQ ID NO:1, and has an activity of regulating an expression of the polynucleotide.
(11) A polynucleotide comprising 10 to 200 continuous bases in the nucleotide sequence of the polynucleotide of any one of (7) to (10), or a polynucleotide comprising a nucleotide sequence complementary to the polynucleotide comprising 10 to 200 continuous based.
(12) A recombinant DNA comprising the polynucleotide of any one of (8) to (11).
(13) A transformant comprising the polynucleotide of any one of (8) to (11) or the recombinant DNA of (12).
(14) A method for producing a polypeptide, comprising:

culturing the transformant of (13) in a medium to produce and accumulate a polypeptide encoded by the polynucleotide of (8) or (9) in the medium, and
recovering the polypeptide from the medium.

(15) A method for producing at least one of an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid, and analogues thereof, comprising:

culturing the transformant of (13) in a medium to produce and accumulate at least one of an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid, and analogues thereof in the medium, and
recovering the at least one of the amino acid, the nucleic acid, the vitamin, the saccharide, the organic acid, and analogues thereof from the medium.

(16) A polypeptide encoded by a polynucleotide comprising the nucleotide sequence selected from SEQ ID NOS:2 to 3431.
(17) A polypeptide comprising the amino acid sequence selected from SEQ ID NOS:3502 to 6931.
(18) The polypeptide according to (16) or (17), wherein at least one amino acid is deleted, replaced, inserted or

added, said polypeptides having an activity which is substantially the same as that of the polypeptide without said at least one amino acid deletion, replacement, insertion or addition.

(19) A polypeptide comprising an amino acid sequence having a homology of at least 60% with the amino acid sequence of the polypeptide of (16) or (17), and having an activity which is substantially the same as that of the polypeptide.

(20) An antibody which recognizes the polypeptide of any one of (16) to (19).

(21) A polypeptide array, comprising:

at least one polypeptide or partial fragment polypeptide selected from the polypeptides of (16) to (19) and partial fragment polypeptides of the polypeptides, and
a solid support adhered thereto.

(22) A polypeptide array, comprising:

at least one antibody which recognizes a polypeptide or partial fragment polypeptide selected from the polypeptides of (16) to (19) and partial fragment polypeptides of the polypeptides, and
a solid support adhered thereto.

(23) A system based on a computer for identifying a target sequence or a target structure motif derived from a coryneform bacterium, comprising the following:

(i) a user input device that inputs at least one nucleotide sequence information selected from SEQ ID NOS:1 to 3501, and target sequence or target structure motif information;
(ii) a data storage device for at least temporarily storing the input information;
(iii) a comparator that compares the at least one nucleotide sequence information selected from SEQ ID NOS: 1 to 3501 with the target sequence or target structure motif information, recorded by the data storage device for screening and analyzing nucleotide sequence information which is coincident with or analogous to the target sequence or target structure motif information; and
(iv) an output device that shows a screening or analyzing result obtained by the comparator.

(24) A method based on a computer for identifying a target sequence or a target structure motif derived from a coryneform bacterium, comprising the following:

(i) inputting at least one nucleotide sequence information selected from SEQ ID NOS:1 to 3501, target sequence information or target structure motif information into a user input device;
(ii) at least temporarily storing said information;
(iii) comparing the at least one nucleotide sequence information selected from SEQ ID NOS:1 to 3501 with the target sequence or target structure motif information; and
(iv) screening and analyzing nucleotide sequence information which is coincident with or analogous to the target sequence or target structure motif information.

(25) A system based on a computer for identifying a target sequence or a target structure motif derived from a coryneform bacterium, comprising the following:

(i) a user input device that inputs at least one amino acid sequence information selected from SEQ ID NOS: 3502 to 7001, and target sequence or target structure motif information;
(ii) a data storage device for at least temporarily storing the input information;
(iii) a comparator that compares the at least one amino acid sequence information selected from SEQ ID NOS: 3502 to 7001 with the target sequence or target structure motif information, recorded by the data storage device for screening and analyzing amino acid sequence information which is coincident with or analogous to the target sequence or target structure motif information; and
(iv) an output device that shows a screening or analyzing result obtained by the comparator.

(26) A method based on a computer for identifying a target sequence or a target structure motif derived from a coryneform bacterium, comprising the following:

(i) inputting at least one amino acid sequence information selected from SEQ ID NOS:3502 to 7001, and target sequence information or target structure motif information into a user input device;

(ii) at least temporarily storing said information;
(iii) comparing the at least one amino acid sequence information selected from SEQ ID NOS 3502 to 7001 with the target sequence or target structure motif information; and
(iv) screening and analyzing amino acid sequence information which is coincident with or analogous to the target sequence or target structure motif information.

(27) A system based on a computer for determining a function of a polypeptide encoded by a polynucleotide having a target nucleotide sequence derived from a coryneform bacterium, comprising the following:

(i) a user input device that inputs at least one nucleotide sequence information selected from SEQ ID NOS 2 to 3501, function information of a polypeptide encoded by the nucleotide sequence, and target nucleotide sequence information;
(ii) a data storage device for at least temporarily storing the input information;
(iii) a comparator that compares the at least one nucleotide sequence information selected from SEQ ID NOS: 2 to 3501 with the target nucleotide sequence information, and determining a function of a polypeptide encoded by a polynucleotide having the target nucleotide sequence which is coincident with or analogous to the polynucleotide having at least one nucleotide sequence selected from SEQ ID NOS:2 to 3501; and
(iv) an output devices that shows a function obtained by the comparator.

(28) A method based on a computer for determining a function of a polypeptide encoded by a polypeptide encoded by a polynucleotide having a target nucleotide sequence derived from a coryneform bacterium, comprising the following:

(i) inputting at least one nucleotide sequence information selected from SEQ ID NOS:2 to 3501, function information of a polypeptide encoded by the nucleotide sequence, and target nucleotide sequence information;
(ii) at least temporarily storing said information;
(iii) comparing the at least one nucleotide sequence information selected from SEQ ID NOS:2 to 3501 with the target nucleotide sequence information; and
(iv) determining a function of a polypeptide encoded by a polynucleotide having the target nucleotide sequence which is coincident with or analogous to the polynucleotide having at least one nucleotide sequence selected from SEQ ID NOS:2 to 3501.

(29) A system based on a computer for determining a function of a polypeptide having a target amino acid sequence derived from a coryneform bacterium, comprising the following:

(i) a user input device that inputs at least one amino acid sequence information selected from SEQ ID NOS: 3502 to 7001, function information based on the amino acid sequence, and target amino acid sequence information;
(ii) a data storing device for at least temporarily storing the input information;
(iii) a comparator that compares the at least one amino acid sequence information selected from SEQ ID NOS: 3502 to 7001 with the target amino acid sequence information for determining a function of a polypeptide having the target amino acid sequence which is coincident with or analogous to the polypeptide having at least one amino acid sequence selected from SEQ ID NOS:3502 to 7001; and
(iv) an output device that shows a function obtained by the comparator.

(30) A method based on a computer for determining a function of a polypeptide having a target amino acid sequence derived from a coryneform bacterium, comprising the following:

(i) inputting at least one amino acid sequence information selected from SEQ ID NOS:3502 to 7001, function information based on the amino acid sequence, and target amino acid sequence information;
(ii) at least temporarily storing said information;
(iii) comparing the at least one amino acid sequence information selected from SEQ ID NOS 3502 to 7001 with the target amino acid sequence information; and
(iv) determining a function of a polypeptide having the target amino acid sequence which is coincident with or analogous to the polypeptide having at least one amino acid sequence selected from SEQ ID NOS:3502 to 7001.

(31) The system according to any one of (23), (25), (27) and (29), wherein a coryneform bacterium is a microor-

ganism of the genus *Corynebacterium*, the genus *Brevibacterium*, or the genus *Microbacterium*.
(32) The method according to any one of (24), (26), (28) and (30), wherein a coryneform bacterium is a microorganism of the genus *Corynebacterium*, the genus *Brevibacterium*, or the genus *Microbacterium*.
(33) The system according to (31), wherein the microorganism belonging to the genus *Corynebacterium* is selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *corynebacterium callunae*, *corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, and *Corynebacterium ammoniagenes*.
(34) The method according to (32), wherein the microorganism belonging to the genus *Corynebacterium* is selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium callunae*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, and *Corynebacterium ammoniagenes*.
(35) A recording medium or storage device which is readable by a computer in which at least one nucleotide sequence information selected from SEQ ID NOS:1 to 3501 or function information based on the nucleotide sequence is recorded, and is usable in the system of (23) or (27) or the method of (24) or (28).
(36) A recording medium or storage device which is readable by a computer in which at least one amino acid sequence information selected from SEQ ID NOS:3502 to 7001 or function information based on the amino acid sequence is recorded, and is usable in the system of (25) or (29) or the method of (26) or (30).
(37) The recording medium or storage device according to
(35) or (36), which is a computer readable recording medium selected from the group consisting of a floppy disc, a hard disc, a magnetic tape, a random access memory (RAM), a read only memory (ROM), a magneto-optic disc (MO), CD-ROM, CD-R, CD-RW, DVD-ROM, DVD-RAM and DVD-RW.
(38) A polypeptide having a homoserine dehydrogenase activity, comprising an amino acid sequence in which the Val residue at the 59th in the amino acid sequence of homoserine dehydrogenase derived from a coryneform bacterium is replaced with an amino acid residue other than a Val residue.
(39) A polypeptide comprising an amino acid sequence in which the Val residue at the 59th position in the amino acid sequence as represented by SEQ ID NO:6952 is replaced with an amino acid residue other than a Val residue.
(40) The polypeptide according to (38) or (39), wherein the Val residue at the 59th position is replaced with an Ala residue.
(41) A polypeptide having pyruvate carboxylase activity, comprising an amino acid sequence in which the Pro residue at the 458th position in the amino acid sequence of pyruvate carboxylase derived from a coryneform bacterium is replaced with an amino acid residue other than a Pro residue.
(42) A polypeptide comprising an amino acid sequence in which the Pro residue at the 458th position in the amino acid sequence represented by SEQ ID NO:4265 is replaced with an amino acid residue other than a Pro residue.
(43) The polypeptide according to (41) or (42), wherein the Pro residue at the 458th position is replaced with a Ser residue.
(44) The polypeptide according to any one of (38) to (43), which is derived from *Corynebacterium glutamicum*.
(45) A DNA encoding the polypeptide of any one of (38) to (44).
(46) A recombinant DNA comprising the DNA of (45).
(47) A transformant comprising the recombinant DNA of (46).
(48) A transformant comprising in its chromosome the DNA of (45).
(49) The transformant according to (47) or (48), which is derived from a coryneform bacterium.
(50) The transformant according to (49), which is derived from *Corynebacterium glutamicum*.
(51) A method for producing L-lysine, comprising:

culturing the transformant of any one of (47) to (50) in a medium to produce and accumulate L-lysine in the medium, and
recovering the L-lysine from the culture.

(52) A method for breeding a coryneform bacterium using the nucleotide sequence information represented by SEQ ID NOS:1 to 3431, comprising the following:

(i) comparing a nucleotide sequence of a genome or gene of a production strain derived a coryneform bacterium which has been subjected to mutation breeding so as to produce at least one compound selected from an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid, and analogous thereof by a fermentation method, with a corresponding nucleotide sequence in SEQ ID NOS:1 to 3431;
(ii) identifying a mutation point present in the production strain based on a result obtained by (i);
(iii) introducing the mutation point into a coryneform bacterium which is free of the mutation point; and
(iv) examining productivity by the fermentation method of the compound selected in (i) of the coryneform

bacterium obtained in (iii)

(53) The method according to (52) wherein the gene is a gene encoding an enzyme in a biosynthetic pathway or a signal transmission pathway

(54) The method according to (52), wherein the mutation point is a mutation point relating to a useful mutation which improves or stabilizes the productivity.

(55) A method for breading a coryneform bacterium using the nucleotide sequence information represented by SEQ ID NOS:1 to 3431, comprising:

(i) comparing a nucleotide sequence of a genome or gene of a production strain derived a coryneform bacterium which has been subjected to mutation breeding so as to produce at least one compound selected from an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid, and analogous thereof by a fermentation method, with a corresponding nucleotide sequence in SEQ ID NOS:1 to 3431;
(ii) identifying a mutation point present in the production strain based on a result obtain by (i);
(iii) deleting a mutation point from a coryneform bacterium having the mutation point; and
(iv) examining productivity by the fermentation method of the compound selected in (i) of the coryneform bacterium obtained in (iii).

(56) The method according to (55) wherein the gene is a gene encoding an enzyme in a biosynthetic pathway or a signal transmission pathway.

(57) The method according to (55), wherein the mutation point is a mutation point which decreases or destabilizes the productivity.

(58) A method for breeding a coryneform bacterium using the nucleotide sequence information represented by SEQ ID NOS:2 to 3431, comprising the following:

(i) identifying an isozyme relating to biosynthesis of at least one compound selected from an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid, and analogous thereof, based on the nucleotide sequence information represented by SEQ ID NOS:2 to 3431;
(ii) classifying the isozyme identified in (i) into an isozyme having the same activity;
(iii) mutating all genes encoding the isozyme having the same activity simultaneously; and
(iv) examining productivity by a fermentation method of the compound selected in (i) of the coryneform bacterium which have been transformed with the gene obtained in (iii).

(59) A method for breeding a coryneform bacterium using the nucleotide sequence information represented by SEQ ID NOS:2 to 3431, comprising the following:

(i) arranging a function information of an open reading frame (ORF) represented by SEQ ID NOS:2 to 3431;
(ii) allowing the arranged ORF to correspond to an enzyme on a known biosynthesis or signal transmission pathway;
(iii) explicating an unknown biosynthesis pathway or signal transmission pathway of a coryneform bacterium in combination with information relating known biosynthesis pathway or signal transmission pathway of a coryneform bacterium;
(iv) comparing the pathway explicated in (iii) with a biosynthesis pathway of a target useful product; and
(v) transgenetically varying a coryneform bacterium based on the nucleotide sequence information to either strengthen a pathway which is judged to be important in the biosynthesis of the target useful product in (iv) or weaken a pathway which is judged not to be important in the biosynthesis of the target useful product in (iv).

(60) A coryneform bacterium, bred by the method of any one of (52) to (59).

(61) The coryneform bacterium according to (60), which is a microorganism belonging to the genus *Corynebacterium*, the genus *Brevibacterium*, or the genus *Microbacterium*.

(62) The coryneform bacterium according to (61), wherein the microorganism belonging to the genus *Corynebacterium* is selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium callunae*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, and *Corynebacterium ammoniagenes*.

(63) A method for producing at least one compound selected from an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid and an analogue thereof, comprising:

culturing a coryneform bacterium of any one of (60) to (62) in a medium to produce and accumulate at least

one compound selected from an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid, and analogues thereof;
recovering the compound from the culture.

(64) The method according to (63), wherein the compound is L-lysine.
(65) A method for identifying a protein relating to useful mutation based on proteome analysis, comprising the following:

(i) preparing

a protein derived from a bacterium of a production strain of a coryneform bacterium which has been subjected to mutation breeding by a fermentation process so as to produce at least one compound selected from an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid, and analogues thereof, and a protein derived from a bacterium of a parent strain of the production strain;

(ii) separating the proteins prepared in (i) by two dimensional electrophoresis;
(iii) detecting the separated proteins, and comparing an expression amount of the protein derived from the production strain with that derived from the parent strain;
(iv) treating the protein showing different expression amounts as a result of the comparison with a peptidase to extract peptide fragments;
(v) analyzing amino acid sequences of the peptide fragments obtained in (iv); and
(vi) comparing the amino acid sequences obtained in (v) with the amino acid sequence represented by SEQ ID NOS:3502 to 7001 to identifying the protein having the amino acid sequences.

As used herein, the term "proteome", which is a coined word by combining "protein" with "genome", refers to a method for examining of a gene at the polypeptide level.
(66) The method according to (65), wherein the coryneform bacterium is a microorganism belonging to the genus *Corynebacterium*, the genus *Brevibacterium*, or the genus *Microbacterium*.
(67) The method according to (66), wherein the microorganism belonging to the genus *Corynebacterium* is selected from the group consisting of *Corynebacterium glutamicum, Corynebacterium acetoacidophilum, Corynebacterium acetoglutamicum, Corynebacterium callunae, corynebacterium herculis, Corynebacterium lilium Corynebacterium melassecola, Corynebacterium thermoaminogenes*, and *Corynebacterium ammoniagenes.*
(68) A biologically pure culture of *Corynebacterium glutamicum* AHP-3 (FERM BP-7382).

[0018] The present invention will be described below in more detail, based on the determination of the full nucleotide sequence of coryneform bacteria.

1. Determination of full nucleotide sequence of coryneform bacteria

[0019] The term "coryneform bacteria" as used herein means a microorganism belonging to the genus *Corynebacterium*, the genus *Brevibacterium* or the genus *Microbacterium* as defined in *Bergeys Manual of Determinative Bacteriology, 8*: 599 (1974).
[0020] Examples include *Corynebacterium acetoacidophilum, Corynebacterium acetoglutamicum, Corynebacterium callunae, Corynebacterium glutamicum, Corynebacterium herculis, Corynebacterium lilium, Corynebacterium melassecola, Corynebacterium thermoaminogenes, Brevibacterium saccharolyticum, Brevibacterium immariophilum, Brevibacterium roseum, Brevibacterium thiogenitalis, Microbacterium ammoniaphilum*, and the like
[0021] Specific examples include *Corynebacterium acetoacidophilum* ATCC 13870, *Corynebacterium acetoglutamicum* ATCC 15806, *Corynebacterium callunae* ATCC 15991, *Corynebacterium glutamicum* ATCC 13032, *Corynebacterium glutamicum* ATCC 13060, *Corynebacterium glutamicum* ATCC 13826 (prior genus and species: *Brevibacterium flavum*, or *Corynebacterium lactofermentum), Corynebacterium glutamicum* ATCC 14020 (prior genus and species: *Brevibacterium divaricatum), Corynebacterium glutamicum* ATCC 13869 (prior genus and species: *Brevibacterium lactofermentum), Corynebacterium herculis* ATCC 13868, *Corynebacterium lilium* ATCC 15990, *Corynebacterium melassecola* ATCC 17965, *Corynebacterium thermoaminogenes FERM* 9244, *Brevibacterium saccharolyticum* ATCC 14066, *Brevibacterium immariophilum* ATCC 14068, *Brevibacterium roseum* ATCC 13825, *Brevibacterium thiogenitalis* ATCC 19240, *Microbacterium ammoniaphilum* ATCC 15354, and the like.

(1) Preparation of genome DNA of coryneform bacteria

[0022] Coryneform bacteria can be cultured by a conventional method

[0023] Any of a natural medium and a synthetic medium can be used, so long as it is a medium suitable for efficient culturing of the microorganism, and it contains a carbon source, a nitrogen source, an inorganic salt, and the like which can be assimilated by the microorganism.

[0024] In *Corynebacterium glutamicum*, for example, a BY medium (7 g/l meat extract, 10 g/l peptone, 3 g/l sodium chloride, 5 g/l yeast extract, pH 7.2) containing 1% of glycine and the like can be used. The culturing is carried out at 25 to 35°C overnight.

[0025] After the completion of the culture, the cells are recovered from the culture by centrifugation. The resulting cells are washed with a washing solution.

[0026] Examples of the washing solution include STE buffer (10.3% sucrose, 25 mmol/l Tris hydrochloride, 25 mmol/l ethylenediaminetetraacetic acid (hereinafter referred to as "EDTA"), pH 8.0), and the like.

[0027] Genome DNA can be obtained from the washed cells according to a conventional method for obtaining genome DNA, namely, lysing the cell wall of the cells using a lysozyme and a surfactant (SDS, *etc.*), eliminating proteins and the like using a phenol solution and a phenol/chloroform solution, and then precipitating the genome DNA with ethanol or the like. Specifically, the following method can be illustrated.

[0028] The washed cells are suspended in a washing solution containing 5 to 20 mg/l lysozyme. After shaking, 5 to 20% SDS is added to lyse the cells. In usual, shaking is gently performed at 25 to 40°C for 30 minutes to 2 hours. After shaking, the suspension is maintained at 60 to 70°C for 5 to 15 minutes for the lysis.

[0029] After the lysis, the suspension is cooled to ordinary temperature, and 5 to 20 ml of Tris-neutralized phenol is added thereto, followed by gently shaking at room temperature for 15 to 45 minutes.

[0030] After shaking, centrifugation (15,000 × g, 20 minutes, 20°C) is carried out to fractionate the aqueous layer.

[0031] After performing extraction with phenol/chloroform and extraction with chloroform (twice) in the same manner, 3 mol/l sodium acetate solution (pH 5.2) and isopropanol are added to the aqueous layer at 1/10 times volume and 2 times volume, of the aqueous layer, respectively, followed by gently stirring to precipitate the genome DNA.

[0032] The genome DNA is dissolved again in a buffer containing 0.01 to 0.04 mg/ml RNase. As an example of the buffer, TE buffer (10 mmol/l Tris hydrochloride, 1 mol/l EDTA, pH 8.0) can be used. After dissolving, the resultant solution is maintained at 25 to 40°C for 20 to 50 minutes and then extracted successively with phenol, phenol/chloroform and chloroform as in the above case.

[0033] After the extraction, isopropanol precipitation is carried out and the resulting DNA precipitate is washed with 70% ethanol, followed by air drying, and then dissolved in TE buffer to obtain a genome DNA solution.

(2) Production of shotgun library

[0034] A method for produce a genome DNA library using the genome DNA of the coryneform bacteria prepared in the above (1) include a method described in *Molecular Cloning, A laboratory Manual*, Second Edition (1989) (hereinafter referred to as "*Molecular Cloning*, 2nd ed."). In particular, the following method can be exemplified to prepare a genome DNA library appropriately usable in determining the full nucleotide sequence by the shotgun method.

[0035] To 0.01 mg of the genome DNA of the coryneform bacteria prepared in the above (1), a buffer, such as TE buffer or the like, is added to give a total volume of 0.4 ml. Then, the genome DNA is digested into fragments of 1 to 10 kb with a sonicator (Yamato Powersonic Model 50). The treatment with the sonicator is performed at an output of 20 continuously for 5 seconds.

[0036] The resulting genome DNA fragments are blunt-ended using DNA blunting kit (manufactured by Takara Shuzo) or the like.

[0037] The blunt-ended genome fragments are fractionated by agarose gel or polyacrylamide gel electrophoresis and genome fragments of 1 to 2 kb are cut out from the gel.

[0038] To the gel, 0.2 to 0.5 ml of a buffer for eluting DNA, such as MG elution buffer (0.5 mol/l ammonium acetate, 10 mmol/l magnesium acetate, 1 mmol/l EDTA, 0.1% SDS) or the like, is added, followed by shaking at 25 to 40°C overnight to elute DNA.

[0039] The resulting DNA eluate is treated with phenol/chloroform and then precipitated with ethanol to obtain a genome library insert.

[0040] This insert is ligated into a suitable vector, such as pUC18 *Sma*I/SAP (manufactured by Amersham Pharmacia Biotech) or the like, using T4 ligase (manufactured by Takara Shuzo) or the like. The ligation can be carried out by allowing a mixture to stand at 10 to 20°C for 20 to 50 hours.

[0041] The resulting ligation product is precipitated with ethanol and dissolved in 5 to 20 μl of TE buffer.

[0042] *Escherichia coli* is transformed in accordance with a conventional method using 0.5 to 2 μl of the ligation solution. Examples of the transformation method include the electroporation method using ELECTRO MAX DHIOB

(manufactured by Life Technologies) for *Escherichia coli*. The electroporation method can be carried out under the conditions as described in the manufacturer's instructions.

[0043] The transformed *Escherichia coli* is spread on a suitable selection medium containing agar, for example, LB plate medium containing 10 to 100 mg/l ampicillin (LB medium (10 g/l bactotrypton, 5 g/l yeast extract, 10 g/l sodium chloride, pH 7.0) containing 1.6% of agar) when pUC18 is used as the cloning vector, and cultured therein.

[0044] The transformant can be obtained as colonies formed on the plate medium. In this step, it is possible to select the transformant having the recombinant DNA containing the genome DNA as white colonies by adding X-gal and IPTG (isopropyl-β-thiogalactopyranoside) to the plate medium.

[0045] The transformant is allowed to stand for culturing in a 96-well titer plate to which 0.05 ml of the LB medium containing 0.1 mg/ml of ampicillin has been added in each well. The resulting culture can be used in an experiment of (4) described below. Also, the culture solution can be stored at -80°C by adding 0.05 ml per well of the LB medium containing 20% glycerol to the culture solution, followed by mixing, and the stored culture solution can be used at any time.

(3) Production of cosmid library

[0046] The genome DNA (0.1 mg) of the coryneform bacteria prepared in the above (1) is partially digested with a restriction enzyme, such as *Sau*3AI or the like, and then ultracentrifuged (26,000 rpm, 18 hours, 20°C) under a 10 to 40% sucrose density gradient using a 10% sucrose buffer (1 mol/l Nacl, 20 mmol/l Tris hydrochloride, 5 mmol/l EDTA, 10% sucrose, pH 8.0) and a 40% sucrose buffer (elevating the concentration of the 10% sucrose buffer to 40%).

[0047] After the centrifugation, the thus separated solution is fractionated into tubes in 1 ml per each tube. After confirming the DNA fragment size of each fraction by agarose gel electrophoresis, a fraction rich in DNA fragments of about 40 kb is precipitated with ethanol.

[0048] The resulting DNA fragment is ligated to a cosmid vector having a cohesive end which can be ligated to the fragment. When the genome DNA is partially digested with *Sau*3AI, the partially digested product can be ligated to, for example, the *Bam*HI site of superCos1 (manufactured by Stratagene) in accordance with the manufacture's instructions.

[0049] The resulting ligation product is packaged using a packaging extract which can be prepared by a method described in *Molecular Cloning*, 2nd ed. and then used in transforming *Escherichia coli*. More specifically, the ligation product is packaged using, for example, a commercially available packaging extract, Gigapack III Gold Packaging Extract (manufactured by Stratagene) in accordance with the manufacture's instructions and then introduced into *Escherichia coli* XL-1-BlueMR (manufactured by Stratagene) or the like.

[0050] The thus transformed *Escherichia coli is* spread on an LB plate medium containing ampicillin, and cultured therein.

[0051] The transformant can be obtained as colonies formed on the plate medium.

[0052] The transformant is subjected to standing culture in a 96-well titer plate to which 0.05 ml of the LB medium containing 0.1 mg/ml ampicillin has been added.

[0053] The resulting culture can be employed in an experiment of (4) described below. Also, the culture solution can be stored at -80°C by adding 0.05 ml per well of the LB medium containing 20% glycerol to the culture solution, followed by mixing, and the stored culture solution can be used at any time.

(4) Determination of nucleotide sequence

(4-1) Preparation of template

[0054] The full nucleotide sequence of genome DNA of coryneform bacteria can be determined basically according to the whole genome shotgun method (*Science, 269*: 496-512 (1995)).

[0055] The template used in the whole genome shotgun method can be prepared by PCR using the library prepared in the above (2) (*DNA Research, 5*: 1-9 (1998)).

[0056] Specifically, the template can be prepared as follows.

[0057] The clone derived from the whole genome shotgun library is inoculated by using a replicator (manufactured by GENETIX) into each well of a 96-well plate to which 0.08 ml per well of the LB medium containing 0.1 mg/ml ampicillin has been added, followed by stationarily culturing at 37°C overnight.

[0058] Next, the culture solution is transported, using a copy plate (manufactured by Tokken), into each well of a 96-well reaction plate (manufactured by PE Biosystems) to which 0.025 ml per well of a PCR reaction solution has been added using TaKaRa Ex Taq (manufactured by Takara Shuzo). Then, PCR is carried out in accordance with the protocol by Makino *et al.* (*DNA Research, 5*: 1-9 (1998)) using GeneAmp PCR System 9700 (manufactured by PE Biosystems) to amplify the inserted fragments.

[0059] The excessive primers and nucleotides are eliminated using a kit for purifying a PCR product and the product is used as the template in the sequencing reaction.

[0060] It is also possible to determine the nucleotide sequence using a double-stranded DNA plasmid as a template.

[0061] The double-stranded DNA plasmid used as the template can be obtained by the following method.

[0062] The clone derived from the whole genome shotgun library is inoculated into each well of a 24- or 96-well plate to which 1.5 ml per well of a 2 · YT medium (16 g/l bactotrypton, 10 g/l yeast extract, 5 g/l sodium chloride, pH 7.0) containing 0.05 mg/ml ampicillin has been added, followed by culturing under shaking at 37°C overnight.

[0063] The double-stranded DNA plasmid can be prepared from the culture solution using an automatic plasmid preparing machine KURABO PI-50 (manufactured by Kurabo Industries), a multiscreen (manufactured by Millipore) or the like, according to each protocol.

[0064] To purify the plasmid, Biomek 2000 manufactured by Beckman Coulter and the like can be used.

[0065] The resulting purified double-stranded DNA plasmid is dissolved in water to give a concentration of about 0.1 mg/ml. Then, it can be used as the template in sequencing.

(4-2) Sequencing reaction

[0066] The sequencing reaction can be carried out according to a commercially available sequence kit or the like. A specific method is exemplified below.

[0067] To 6 μl of a solution of ABI PRISM BigDye Terminator Cycle Sequencing Ready Reaction Kit (manufactured by PE Biosystems), 1 to 2 pmol of an M13 regular direction primer (M13-21) or an M13 reverse direction primer (M13REV) (*DNA Research, 5*: 1-9 (1998)) and 50 to 200 ng of the template prepared in the above (4-1) (the PCR product or plasmid) to give 10 μl of a sequencing reaction solution.

[0068] A dye terminator sequencing reaction (35 to 55 cycles) is carried out using this reaction solution and GeneAmp PCR System 9700 (manufactured by PE Biosystems) or the like. The cycle parameter can be determined in accordance with a commercially available kit, for example, the manufacture's instructions attached with ABI PRISM Big Dye Terminator Cycle Sequencing Ready Reaction Kit.

[0069] The sample can be purified using a commercially available product, such as Multi Screen HV plate (manufactured by Millipore) or the like, according to the manufacture's instructions.

[0070] The thus purified reaction product is precipitated with ethanol, dried and then used for the analysis. The dried reaction product can be stored in the dark at -30°C and the stored reaction product can be used at any time.

[0071] The dried reaction product can be analyzed using a commercially available sequencer and an analyzer according to the manufacture's instructions.

[0072] Examples of the commercially available sequencer include ABI PRISM 377 DNA Sequencer (manufactured by PE Biosystems). Example of the analyzer include ABI PRISM 3700 DNA Analyzer (manufactured by PE Biosystems).

(5) Assembly

[0073] A software, such as phred (The University of Washington) or the like, can be used as base call for use in analyzing the sequence information obtained in the above (4). A software, such as Cross_Match (The University of Washington) or SPS Cross_Match (manufactured by Southwest Parallel Software) or the like, can be used to mask the vector sequence information.

[0074] For the assembly, a software, such as phrap (The University of Washington), SPS phrap (manufactured by Southwest Parallel Software) or the like, can be used.

[0075] In the above, analysis and output of the results thereof, a computer such as UNIX, PC, Macintosh, and the like can be used.

[0076] Contig obtained by the assembly can be analyzed using a graphical editor such as consed (The University of Washington) or the like.

[0077] It is also possible to perform a series of the operations from the base call to the assembly in a lump using a script phredPhrap attached to the consed.

[0078] As used herein, software will be understood to also be referred to as a comparator.

(6) Determination of nucleotide sequence in gap part

[0079] Each of the cosmids in the cosmid library constructed in the above (3) is prepared in the same manner as in the preparation of the double-stranded DNA plasmid described in the above (4-1). The nucleotide sequence at the end of the insert fragment of the cosmid is determined using a commercially available kit, such as ABI PRISM BigDye Terminator Cycle Sequencing Ready Reaction Kit (manufactured by PE Biosystems) according to the manufacture's instructions.

[0080] About 800 cosmid clones are sequenced at both ends of the inserted fragment to detect a nucleotide sequence in the contig derived from the shotgun sequencing obtained in (5) which is coincident with the sequence. Thus, the chain linkage between respective cosmid clones and respective contigs are clarified, and mutual alignment is carried out. Furthermore, the results are compared with known physical maps to map the cosmids and the contigs. In case of *Corynebacterium glutamicum* ATCC 13032, a physical map of *Mol. Gen. Genet., 252*: 255-265 (1996) can be used.

[0081] The sequence in the region which cannot be covered with the contigs (gap part) can be determined by the following method.

[0082] Clones containing sequences positioned at the ends of the contigs are selected. Among these, a clone wherein only one end of the inserted fragment has been determined is selected and the sequence at the opposite end of the inserted fragment is determined.

[0083] A shotgun library clone or a cosmid clone derived therefrom containing the sequences at the respective ends of the inserted fragments in the two contigs is identified and the full nucleotide sequence of the inserted fragment of the clone is determined.

[0084] According to this method, the nucleotide sequence of the gap part can be determined.

[0085] When no shotgun library clone or cosmid clone covering the gap part is available, primers complementary to the end sequences of the two different contigs are prepared and the DNA fragment in the gap part is amplified. Then, sequencing is performed by the primer walking method using the amplified DNA fragment as a template or by the shotgun method in which the sequence of a shotgun clone prepared from the amplified DNA fragment is determined. Thus, the nucleotide sequence of the above-described region can be determined.

[0086] In a region showing a low sequence accuracy, primers are synthesized using AUTOFINISH function and NAVIGATING function of consed (The University of Washington), and the sequence is determined by the primer walking method to improve the sequence accuracy.

[0087] Examples of the thus determined nucleotide sequence of the full genome include the full nucleotide sequence of genome of *Corynebacterium glutamicum* ATCC 13032 represented by SEQ ID NO:1.

(7) Determination of nucleotide sequence of microorganism genome DNA using the nucleotide sequence represented by SEQ ID NO:1

[0088] A nucleotide sequence of a polynucleotide having a homology of 80% or more with the full nucleotide sequence of *Corynebacterium glutamicum* ATCC 13032 represented by SEQ ID NO:1 as determined above can also be determined using the nucleotide sequence represented by SEQ ID NO:1, and the polynucleotide having a nucleotide sequence having a homology of 80% or more with the nucleotide sequence represented by SEQ ID NO:1 of the present invention is within the scope of the present invention. The term "polynucleotide having a nucleotide sequence having a homology of 80% or more with the nucleotide sequence represented by SEQ ID NO:1 of the present invention" is a polynucleotide in which a full nucleotide sequence of the chromosome DNA can be determined using as a primer an oligonucleotide composed of continuous 5 to 50 nucleotides in the nucleotide sequence represented by SEQ ID NO: 1, for example, according to PCR using the chromosome DNA as a template. A particularly preferred primer in determination of the full nucleotide sequence is an oligonucleotide having nucleotide sequences which are positioned at the interval of about 300 to 500 bp, and among such oligonucleotides, an oligonucleotide having a nucleotide sequence selected from DNAs encoding a protein relating to a main metabolic pathway is particularly preferred. The polynucleotide in which the full nucleotide sequence of the chromosome DNA can be determined using the oligonucleotide includes polynucleotides constituting a chromosome DNA derived from a microorganism belonging to coryneform bacteria. Such a polynucleotide is preferably a polynucleotide constituting chromosome DNA derived from a microorganism belonging to the genus *Corynebacterium*, more preferably a polynucleotide constituting a chromosome DNA of *Corynebacterium glutamicum*.

2. Identification of ORF (open reading frame) and expression regulatory fragment and determination of the function of ORF

[0089] Based on the full nucleotide sequence data of the genome derived from coryneform bacteria determined in the above item 1, an ORF and an expression modulating fragment can be identified. Furthermore, the function of the thus determined ORF can be determined.

[0090] The ORF means a continuous region in the nucleotide sequence of mRNA which can be translated as an amino acid sequence to mature to a protein. A region of the DNA coding for the ORF of mRNA is also called ORF.

[0091] The expression modulating fragment (hereinafter referred to as "EMF") is used herein to define a series of polynucleotide fragments which modulate the expression of the ORF or another sequence ligated operatably thereto. The expression "modulate the expression of a sequence ligated operatably" is used herein to refer to changes in the expression of a sequence due to the presence of the EMF. Examples of the EMF include a promoter, an operator, an

enhancer, a silencer, a ribosome-binding sequence, a transcriptional termination sequence, and the like. In coryneform bacteria, an EMF is usually present in an intergenic segment (a fragment positioned between two genes: about 10 to 200 nucleotides in length). Accordingly, an EMF is frequently present in an intergenic segment of 10 nucleotides or longer. It is also possible to determine or discover the presence of an EMF by using known EMF sequences as a target sequence or a target structural motif (or a target motif) using an appropriate software or comparator, such as FASTA (*Proc. Natl. Acad. Sci. USA, 85*: 2444-48 (1988)), BLAST (*J. Mol. Biol., 215*: 403-410 (1990)) or the like. Also, it can be identified and evaluated using a known EMF-capturing vector (for example, pKK232-8: manufactured by Amersham Pharmacia Biotech).

[0092] The term "target sequence" is used herein to refer to a nucleotide sequence composed of 6 or more nucleotides, an amino acid sequence composed of 2 or more amino acids, or a nucleotide sequence encoding this amino acid sequence composed of 2 or more amino acids. A longer target sequence appears at random in a data base at the lower possibility. The target sequence is preferably about 10 to 100 amino acid residues or about 30 to 300 nucleotide residues.

[0093] The term "target structural motif" or "target motif" is used herein to refer to a sequence or a combination of sequences selected optionally and reasonably. Such a motif is selected on the basis of the threedimensional structure formed by the folding of a polypeptide by means known to one of ordinary skill in the art. Various motives are known.

[0094] Examples of the target motif of a polypeptide include, but are not limited to, an enzyme activity site, a protein-protein interaction site, a signal sequence, and the like. Examples of the target motif of a nucleic acid include a promoter sequence, a transcriptional regulatory factor binding sequence, a hair pin structure, and the like.

[0095] Examples of highly useful EMF include a high-expression promoter, an inducible-expression promoter, and the like. Such an EMF can be obtained by positionally determining the nucleotide sequence of a gene which is known or expected as achieving high expression (for example, ribosomal RNA gene: GenBank Accession No. M16175 or Z46753) or a gene showing a desired induction pattern (for example, isocitrate lyase gene induced by acetic acid: Japanese Published Unexamined Patent Application No. 56782/93) via the alignment with the full genome nucleotide sequence determined in the above item 1, and isolating the genome fragment in the upstream part (usually 200 to 500 nucleotides from the translation initiation site). It is also possible to obtain a highly useful EMF by selecting an EMF showing a high expression efficiency or a desired induction pattern from among promoters captured by the EMF-capturing vector as described above.

[0096] The ORF can be identified by extracting characteristics common to individual ORFs, constructing a general model based on these characteristics, and measuring the conformity of the subject sequence with the model. In the identification, a software, such as GeneMark (*Nuc. Acids. Res., 22*: 4756-67 (1994): manufactured by GenePro)), GeneMark.hmm (manufactured by GenePro), GeneHacker (*Protein, Nucleic Acid and Enzyme, 42*: 3001-07 (1997)), Glimmer (*Nuc. Acids. Res., 26*: 544-548 (1998): manufactured by The Institute of Genomic Research), or the like, can be used. In using the software, the default (initial setting) parameters are usually used, though the parameters can be optionally changed.

[0097] In the above-described comparisons, a computer, such as UNIX, PC, Macintosh, or the like, can be used.

[0098] Examples of the ORF determined by the method of the present invention include ORFs having the nucleotide sequences represented by SEQ ID NOS:2 to 3501 present in the genome of *Corynebacterium glutamicum* as represented by SEQ ID NO:1. In these ORFs, polypeptides having the amino acid sequences represented by SEQ ID NOS: 3502 to 7001 are encoded.

[0099] The function of an ORF can be determined by comparing the identified amino acid sequence of the ORF with known homologous sequences using a homology searching software or comparator, such as BLAST, FAST, Smith & Waterman (*Meth. Enzym., 164*: 765 (1988)) or the like on an amino acid data base, such as Swith-Prot, PIR, GenBank-nr-aa, GenPept constituted by protein-encoding domains derived from GenBank data base, OWL or the like.

[0100] Furthermore, by the homology searching, the identity and similarity with the amino acid sequences of known proteins can also be analyzed.

[0101] With respect of the term "identity" used herein, where two polypeptides each having 10 amino acids are different in the positions of 3 amino acids, these polypeptides have an identity of 70% with each other. In case wherein one of the different 3 amino acids is analogue (for example, leucine and isoleucine), these polypeptides have a similarity of 80%.

[0102] As a specific example, Table 1 shows the registration numbers in known data bases of sequences which are judged as having the highest similarity with the nucleotide sequence of the ORF derived from *Corynebacterium glutamicum* ATCC 13032, genes of these sequences, functions of these genes, and identities thereof compared with known amino acid translation sequences.

[0103] Thus, a great number of novel genes derived from coryneform bacteria can be identified by determining the full nucleotide sequence of the genome derived from coryneform bacterium by the means of the present invention. Moreover, the function of the proteins encoded by these genes can be determined. Since coryneform bacteria are industrially highly useful microorganisms, many of the identified genes are industrially useful.

[0104] Moreover, the characteristics of respective microorganisms can be clarified by classifying the functions thus determined. As a result, valuable information in breeding is obtained.

[0105] Furthermore, from the ORF information derived from coryneform bacteria, the ORF corresponding to the microorganism is prepared and obtained according to the general method as disclosed in *Molecular Cloning*, 2nd ed. or the like. Specifically, an oligonucleotide having a nucleotide sequence adjacent to the ORF is synthesized, and the ORF can be isolated and obtained using the oligonucleotide as a primer and a chromosome DNA derived from coryneform bacteria as a template according to the general PCR cloning technique. Thus obtained ORF sequences include polynucleotides comprising the nucleotide sequence represented by any one of SEQ ID NOS:2 to 3501.

[0106] The ORF or primer can be prepared using a polypeptide synthesizer based on the above sequence information.

[0107] Examples of the polynucleotide of the present invention include a polynucleotide containing the nucleotide sequence of the ORF obtained in the above, and a polynucleotide which hybridizes with the polynucleotide under stringent conditions.

[0108] The polynucleotide of the present invention can be a single-stranded DNA, a double-stranded DNA and a single-stranded RNA, though it is not limited thereto.

[0109] The polynucleotide which hybridizes with the polynucleotide containing the nucleotide sequence of the ORF obtained in the above under stringent conditions includes a degenerated mutant of the ORF. A degenerated mutant is a polynucleotide fragment having a nucleotide sequence which is different from the sequence of the ORF of the present invention which encodes the same amino acid sequence by degeneracy of a gene code.

[0110] Specific examples include a polynucleotide comprising the nucleotide sequence represented by any one of SEQ ID NOS:2 to 3431, and a polynucleotide which hybridizes with the polynucleotide under stringent conditions.

[0111] A polynucleotide which hybridizes under stringent conditions is a polynucleotide obtained by colony hybridization, plaque hybridization, Southern blot hybridization or the like using, as a probe, the polynucleotide having the nucleotide sequence of the ORF identified in the above. Specific examples include a polynucleotide which can be identified by carrying out hybridization at 65°C in the presence of 0.7-1.0 M NaCl using a filter on which a polynucleotide prepared from colonies or plaques is immobilized, and then washing the filter with 0.1x to 2x SSC solution (the composition of Ix SSC contains 150 mM sodium chloride and 15 mM sodium citrate) at 65°C.

[0112] The hybridization can be carried out in accordance with known methods described in, for example, *Molecular Cloning*, 2nd ed., *Current Protocols in Molecular Biology, DNA Cloning 1: Core Techniques, A Practical Approach*, Second Edition, Oxford University (1995) or the like. Specific examples of the polynucleotide which can be hybridized include a DNA having a homology of 60% or more, preferably 80% or more, and particularly preferably 95% or more, with the nucleotide sequence represented by any one of SEQ ID NO:2 to 3431 when calculated using default (initial setting) parameters of a homology searching software, such as BLAST, FASTA, Smith-Waterman or the like.

[0113] Also, the polynucleotide of the present invention includes a polynucleotide encoding a polypeptide comprising the amino acid sequence represented by any one of SEQ ID NOS:3502 to 6931 and a polynucleotide which hybridizes with the polynucleotide under stringent conditions.

[0114] Furthermore, the polynucleotide of the present invention includes a polynucleotide which is present in the 5' upstream or 3' downstream region of a polynucleotide comprising the nucleotide sequence of any one of SEQ ID NOS: 2 to 3431 in a polynucleotide comprising the nucleotide sequence represented by SEQ ID NO:1, and has an activity of regulating an expression of a polypeptide encoded by the polynucleotide. Specific examples of the polynucleotide having an activity of regulating an expression of a polypeptide encoded by the polynucleotide includes a polynucleotide encoding the above described EMF, such as a promoter, an operator, an enhancer, a silencer, a ribosome-binding sequence, a transcriptional termination sequence, and the like.

[0115] The primer used for obtaining the ORF according to the above PCR cloning technique includes an oligonucleotide comprising a sequence which is the same as a sequence of 10 to 200 continuous nucleotides in the nucleotide sequence of the ORF and an adjacent region or an oligonucleotide comprising a sequence which is complementary to the oligonucleotide. Specific examples include an oligonucleotide comprising a sequence which is the same as a sequence of 10 to 200 continuous nucleotides of the nucleotide sequence represented by any one of SEQ ID NOS:1 to 3431, and an oligonucleotide comprising a sequence complementary to the oligonucleotide comprising a sequence of at least 10 to 20 continuous nucleotide of any one of SEQ ID NOS:1 to 3431. When the primers are used as a sense primer and an antisense primer, the above-described oligonucleotides in which melting temperature (T_m) and the number of nucleotides are not significantly different from each other are preferred.

[0116] The oligonucleotide of the present invention includes an oligonucleotide comprising a sequence which is the same as 10 to 200 continuous nucleotides of the nucleotide sequence represented by any one of SEQ ID NOS:1 to 3431 or an oligonucleotide comprising a sequence complementary to the oligonucleotide.

[0117] Also, analogues of these oligonucleotides (hereinafter also referred to as "analogous oligonucleotides") are also provided by the present invention and are useful in the methods described herein.

[0118] Examples of the analogous oligonucleotides include analogous oligonucleotides in which a phosphodiester

bond in an oligonucleotide is converted to a phosphorothioate bond, analogous oligonucleotides in which a phosphodiester bond in an oligonucleotide is converted to an N3'-P5' phosphoamidate bond, analogous oligonucleotides in which ribose and a phosphodiester bond in an oligonucleotide is converted to a peptide nucleic acid bond, analogous oligonucleotides in which uracil in an oligonucleotide is replaced with C-5 propynyluracil, analogous oligonucleotides in which uracil in an oligonucleotide is replaced with C-5 thiazoluracil, analogous oligonucleotides in which cytosine in an oligonucleotide is replaced with C-5 propynylcytosine, analogous oligonucleotides in which cytosine in an oligonucleotide is replaced with phenoxazine-modified cytosine, analogous oligonucleotides in which ribose in an oligonucleotide is replaced with 2'-O-propylribose, analogous oligonucleotides in which ribose in an oligonucleotide is replaced with 2'-methoxyethoxyribose, and the like (*Cell Engineering*, *16*: 1463 (1997)).

[0119] The above oligonucleotides and analogous oligonucleotides of the present invention can be used as probes for hybridization and antisense nucleic acids described below in addition to as primers.

[0120] Examples of a primer for the antisense nucleic acid techniques known in the art include an oligonucleotide which hybridizes the oligonucleotide of the present invention under stringent conditions and has an activity regulating expression of the polypeptide encoded by the polynucleotide, in addition to the above oligonucleotide.

3. Determination of isozymes

[0121] Many mutants of coryneform bacteria which are useful in the production of useful substances, such as amino acids, nucleic acids, vitamins, saccharides, organic acids, and the like, are obtained by the present invention.

[0122] However, since the gene sequence data of the microorganism has been, to date, insufficient, useful mutants have been obtained by mutagenic techniques using a mutagen, such as nitrosoguanidine (NTG) or the like

[0123] Although genes can be mutated randomly by the mutagenic method using the above-described mutagen, all genes encoding respective isozymes having similar properties relating to the metabolism of intermediates cannot be mutated. In the mutagenic method using a mutagen, genes are mutated randomly. Accordingly, harmful mutations worsening culture characteristics, such as delay in growth, accelerated foaming, and the like, might be imparted at a great frequency, in a random manner.

[0124] However, if gene sequence information is available, such as is provided by the present invention, it is possible to mutate all of the genes encoding target isozymes. In this case, harmful mutations may be avoided and the target mutation can be incorporated.

[0125] Namely, an accurate number and sequence information of the target isozymes in coryneform bacteria can be obtained based on the ORF data obtained in the above item 2. By using the sequence information, all of the target isozyme genes can be mutated into genes having the desired properties by, for example, the site-specific mutagenesis method described in *Molecular Cloning*, 2nd ed. to obtain useful mutants having elevated productivity of useful substances.

4. Clarification or determination of biosynthesis pathway and signal transmission pathway

[0126] Attempts have been made to elucidate biosynthesis pathways and signal transmission pathways in a number of organisms, and many findings have been reported. However, there are many unknown aspects of coryneform bacteria since a number of genes have not been identified so far.

[0127] These unknown points can be clarified by the following method.

[0128] The functional information of ORF derived from coryneform bacteria as identified by the method of above item 2 is arranged. The term "arranged" means that the ORF is classified based on the biosynthesis pathway of a substance or the signal transmission pathway to which the ORF belongs using known information according to the functional information. Next, the arranged ORF sequence information is compared with enzymes on the biosynthesis pathways or signal transmission pathways of other known organisms. The resulting information is combined with known data on coryneform bacteria. Thus, the biosynthesis pathways and signal transmission pathways in coryneform bacteria, which have been unknown so far, can be determined.

[0129] As a result that these pathways which have been unknown or unclear hitherto are clarified, a useful mutant for producing a target useful substance can be efficiently obtained.

[0130] When the thus clarified pathway is judged as important in the synthesis of a useful product, a useful mutant can be obtained by selecting a mutant wherein this pathway has been strengthened. Also, when the thus clarified pathway is judged as not important in the biosynthesis of the target useful product, a useful mutant can be obtained by selecting a mutant wherein the utilization frequency of this pathway is lowered

5. Clarification or determination of useful mutation point

[0131] Many useful mutants of coryneform bacteria which are suitable for the production of useful substances, such

as amino acids, nucleic acids, vitamins, saccharides, organic acids, and the like, have been obtained. However, it is hardly known which mutation point is imparted to a gene to improve the productivity.

[0132] However, mutation points contained in production strains can be identified by comparing desired sequences of the genome DNA of the production strains obtained from coryneform bacteria by the mutagenic technique with the nucleotide sequences of the corresponding genome DNA and ORF derived from coryneform bacteria determined by the methods of the above items 1 and 2 and analyzing them.

[0133] Moreover, effective mutation points contributing to the production can be easily specified from among these mutation points on the basis of known information relating to the metabolic pathways, the metabolic regulatory mechanisms, the structure activity correlation of enzymes, and the like.

[0134] When any efficient mutation can be hardly specified based on known data, the mutation points thus identified can be introduced into a wild strain of coryneform bacteria or a production strain free of the mutation. Then, it is examined whether or not any positive effect can be achieved on the production.

[0135] For example, by comparing the nucleotide sequence of homoserine dehydrogenase gene *hom* of a lysine-producing B-6 strain of *Corynebacterium glutamicum* (*Appl. Microbiol. Biotechnol., 32*: 269-273 (1989)) with the nucleotide sequence corresponding to the genome of *Corynebacterium glutamicum* ATCC 13032 according to the present invention, a mutation of amino acid replacement in which valine at the 59-position is replaced with alanine (Val59Ala) was identified. A strain obtained by introducing this mutation into the ATCC 13032 strain by the gene replacement method can produce lysine, which indicates that this mutation is an effective mutation contributing to the production of lysine.

[0136] Similarly, by comparing the nucleotide sequence of pyruvate carboxylase gene *pyc* of the B-6 strain with the nucleotide sequence corresponding to the ATCC 13032 genome, a mutation of amino acid replacement in which proline at the 458-position was replaced with serine (Pro458Ser) was identified. A strain obtained by introducing this mutation into a lysine-producing strain of No. 58 (FERM BP-7134) of *Corynebacterium glutamicum* free of this mutation shows an improved lysine productivity in comparison with the No. 58 strain, which indicates that this mutation is an effective mutation contributing to the production of lysine.

[0137] In addition, a mutation A1a213Thr in glucose-6-phosphate dehydrogenase was specified as an effective mutation relating to the production of lysine by detecting glucose-6-phosphate dehydrogenase gene *zwf* of the B-6 strain.

[0138] Furthermore, the lysine-productivity of *Corynebacterium glutamicum* was improved by replacing the base at the 932-position of aspartokinase gene *lysC* of the *Corynebacterium glutamicum* ATCC 13032 genome with cytosine to thereby replace threonine at the 311-position by isoleucine, which indicates that this mutation is an effective mutation contributing to the production of lysine.

[0139] Also, as another method to examine whether or not the identified mutation point is an effective mutation, there is a method in which the mutation possessed by the lysine-producing strain is returned to the sequence of a wild type strain by the gene replacement method and whether or not it has a negative influence on the lysine productivity. For example, when the amino acid replacement mutation Val59Ala possessed by *hom* of the lysine-producing B-6 strain was returned to a wild type amino acid sequence, the lysine productivity was lowered in comparison with the B-6 strain. Thus, it was found that this mutation is an effective mutation contributing to the production of lysine.

[0140] Effective mutation points can be more efficiently and comprehensively extracted by combining, if needed, the DNA array analysis or proteome analysis described below.

6. Method of breeding industrially advantageous production strain

[0141] It has been a general practice to construct production strains, which are used industrially in the fermentation production of the target useful substances, such as amino acids, nucleic acids, vitamins, saccharides, organic acids, and the like, by repeating mutagenesis and breeding based on random mutagenesis using mutagens, such as NTG or the like, and screening.

[0142] In recent years, many examples of improved production strains have been made through the use of recombinant DNA techniques. In breeding, however, most of the parent production strains to be improved are mutants obtained by a conventional mutagenic procedure (W. Leuchtenberger, *Amino Acids - Technical Production and Use*, In: Roehr (ed) Biotechnology, second edition, vol. 6, products of primary metabolism, VCH Verlagsgesellschaft mbH, Weinheim, P 465 (1996))

[0143] Although mutagenesis methods have largely contributed to the progress of the fermentation industry, they suffer from a serious problem of multiple, random introduction of mutations into every part of the chromosome. Since many mutations are accumulated in a single chromosome each time a strain is improved, a production strain obtained by the random mutation and selecting is generally inferior in properties (for example, showing poor growth, delayed consumption of saccharides, and poor resistance to stresses such as temperature and oxygen) to a wild type strain, which brings about troubles such as failing to establish a sufficiently elevated productivity, being frequently contaminated with miscellaneous bacteria, requiring troublesome procedures in culture maintenance, and the like, and, in its

turn elevating the production cost in practice. In addition, the improvement in the productivity is based on random mutations and thus the mechanism thereof is unclear. Therefore, it is very difficult to plan a rational breeding strategy for the subsequent improvement in the productivity.

[0144] According to the present invention, effective mutation points contributing to the production can be efficiently specified from among many mutation points accumulated in the chromosome of a production strain which has been bred from coryneform bacteria and, therefore, a novel breeding method of assembling these effective mutations in the coryneform bacteria can be established. Thus, a useful production strain can be reconstructed. It is also possible to construct a useful production strain from a wild type strain.

[0145] Specifically, a useful mutant can be constructed in the following manner.

[0146] One of the mutation points is incorporated into a wild type strain of coryneform bacteria. Then, it is examined whether or not a positive effect is established on the production. When a positive effect is obtained, the mutation point is saved. When no effect is obtained, the mutation point is removed. Subsequently, only a strain having the effective mutation point is used as the parent strain, and the same procedure is repeated. In general, the effectiveness of a mutation positioned upstream cannot be clearly evaluated in some cases when there is a rate-determining point in the downstream of a biosynthesis pathway. It is therefore preferred to successively evaluate mutation points upward from downstream.

[0147] By reconstituting effective mutations by the method as described above in a wild type strain or a strain which has a high growth speed or the same ability to consume saccharides as the wild type strain, it is possible to construct an industrially advantageous strain which is free of troubles in the previous methods as described above and to conduct fermentation production using such strains within a short time or at a higher temperature.

[0148] For example, a lysine-producing mutant B-6 (*Appl. Microbiol. Biotechnol., 32*: 262-273 (1989)), which is obtained by multiple rounds of random mutagenesis from a wild type strain *Corynebacterium glutamicum* ATCC 13032, enables lysine fermentation to be performed at a temperature between 30 and 34°C but shows lowered growth and lysine productivity at a temperature exceeding 34°C. Therefore, the fermentation temperature should be maintained at 34°C or lower. In contrast thereto, the production strain described in the above item 5, which is obtained by reconstituting effective mutations relating to lysine production, can achieve a productivity at 40 to 42°C equal or superior to the result obtained by culturing at 30 to 34°C. Therefore, this strain is industrially advantageous since it can save the load of cooling during the fermentation.

[0149] When culture should be carried out at a high temperature exceeding 43°C, a production strain capable of conducting fermentation production at a high temperature exceeding 43°C can be obtained by reconstituting useful mutations in a microorganism belonging to the genus *Corynebacterium* which can grow at high temperature exceeding 43°C. Examples of the microorganism capable of growing at a high temperature exceeding 43°C include *Corynebacterium thermoaminogenes*, such as *Corynebacterium thermoaminogenes* FERM 9244, FERM 9245, FERM 9246 and FERM 9247.

[0150] A strain having a further improved productivity of the target product can be obtained using the thus reconstructed strain as the parent strain and further breeding it using the conventional mutagenesis method, the gene amplification method, the gene replacement method using the recombinant DNA technique, the transduction method or the cell fusion method. Accordingly, the microorganism of the present invention includes, but is not limited to, a mutant, a cell fusion strain, a transformant, a transductant or a recombinant strain constructed by using recombinant DNA techniques so long as it is a producing strain obtained via the step of accumulating at least two effective mutations in a coryneform bacteria in the course of breeding.

[0151] When a mutation point judged as being harmful to the growth or production is specified, on the other hand, it is examined whether or not the producing strain used at present contains the mutation point. When it has the mutation, it can be returned to the wild type gene and thus a further useful production strain can be bred.

[0152] The breeding method as described above is applicable to microorganisms, other than coryneform bacteria, which have industrially advantageous properties (for example, microorganisms capable of quickly utilizing less expensive carbon sources, microorganisms capable of growing at higher temperatures).

7. Production and utilization of polynucleotide array

(1) Production of polynucleotide array

[0153] A polynucleotide array can be produced using the polynucleotide or oligonucleotide of the present invention obtained in the above items 1 and 2.

[0154] Examples include a polynucleotide array comprising a solid support to which at least one of a polynucleotide comprising the nucleotide sequence represented by SEQ ID NOS:2 to 3501, a polynucleotide which hybridizes with the polynucleotide under stringent conditions, and a polynucleotide comprising 10 to 200 continuous nucleotides in the nucleotide sequence of the polynucleotide is adhered; and a polynucleotide array comprising a solid support to

which at least one of a polynucleotide encoding a polypeptide comprising the amino acid sequence represented by any one of SEQ ID NOS:3502 to 7001, a polynucleotide which hybridizes with the polynucleotide under stringent conditions, and a polynucleotide comprising 10 to 200 continuous bases in the nucleotide sequences of the polynucleotides is adhered.

[0155] Polynucleotide arrays of the present invention include substrates known in the art, such as a DNA chip, a DNA microarray and a DNA macroarray, and the like, and comprises a solid support and plural polynucleotides or fragments thereof which are adhered to the surface of the solid support.

[0156] Examples of the solid support include a glass plate, a nylon membrane, and the like.

[0157] The polynucleotides or fragments thereof adhered to the surface of the solid support can be adhered to the surface of the solid support using the general technique for preparing arrays. Namely, a method in which they are adhered to a chemically surface-treated solid support, for example, to which a polycation such as polylysine or the like has been adhered (*Nat. Genet.*, *21*: 15-19 (1999)). The chemically surface-treated supports are commercially available and the commercially available solid product can be used as the solid support of the polynucleotide array according to the present invention.

[0158] As the polynucleotides or oligonucleotides adhered to the solid support, the polynucleotides and oligonucleotides of the present invention obtained in the above items 1 and 2 can be used.

[0159] The analysis described below can be efficiently performed by adhering the polynucleotides or oligonucleotides to the solid support at a high density, though a high fixation density is not always necessary.

[0160] Apparatus for achieving a high fixation density, such as an arrayer robot or the like, is commercially available from Takara Shuzo (GMS417 Arrayer), and the commercially available product can be used.

[0161] Also, the oligonucleotides of the present invention can be synthesized directly on the solid support by the photolithography method or the like (*Nat. Genet.*, *21*: 20-24 (1999)). In this method, a linker having a protective group which can be removed by light irradiation is first adhered to a solid support, such as a slide glass or the like. Then, it is irradiated with light through a mask (a photolithograph mask) permeating light exclusively at a definite part of the adhesion part. Next, an oligonucleotide having a protective group which can be removed by light irradiation is added to the part. Thus, a ligation reaction with the nucleotide arises exclusively at the irradiated part. By repeating this procedure, oligonucleotides, each having a desired sequence, different from each other can be synthesized in respective parts. Usually, the oligonucleotides to be synthesized have a length of 10 to 30 nucleotides.

(2) Use of polynucleotide array

[0162] The following procedures (a) and (b) can be carried out using the polynucleotide array prepared in the above (1).

(a) Identification of mutation point of coryneform bacterium mutant and analysis of expression amount and expression profile of gene encoded by genome

[0163] By subjecting a gene derived from a mutant of coryneform bacteria or an examined gene to the following steps (i) to (iv), the mutation point of the gene can be identified or the expression amount and expression profile of the gene can be analyzed:

(i) producing a polynucleotide array by the method of the above (1);
(ii) incubating polynucleotides immobilized on the polynucleotide array together with the labeled gene derived from a mutant of the coryneform bacterium using the polynucleotide array produced in the above (i) under hybridization conditions;
(iii) detecting the hybridization; and
(iv) analyzing the hybridization data.

[0164] The gene derived from a mutant of coryneform bacteria or the examined gene include a gene relating to biosynthesis of at least one selected from amino acids, nucleic acids, vitamins, saccharides, organic acids, and analogues thereof.

[0165] The method will be described in detail.

[0166] A single nucleotide polymorphism (SNP) in a human region of 2,300 kb has been identified using polynucleotide arrays (*Science, 280*: 1077-82 (1998)). In accordance with the method of identifying SNP and methods described in *Science, 278*: 680-686 (1997); *Proc. Natl. Acad. Sci. USA, 96*: 12833-38 (1999); *Science, 284*: 1520-23 (1999), and the like using the polynucleotide array produced in the above (1) and a nucleic acid molecule (DNA, RNA) derived from coryneform bacteria in the method of the hybridization, a mutation point of a useful mutant, which is useful in producing an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid, or the like can be identified and the gene

expression amount and the expression profile thereof can be analyzed

[0167] The nucleic acid molecule (DNA, RNA) derived from the coryneform bacteria can be obtained according to the general method described in *Molecular Cloning*, 2nd ed. or the like. mRNA derived from *Corynebacterium glutamicum* can also be obtained by the method of Bormann *et al.* (*Molecular Microbiology*, *6*: 317-326 (1992)) or the like.

[0168] Although ribosomal RNA (rRNA) is usually obtained in large excess in addition to the target mRNA, the analysis is not seriously disturbed thereby.

[0169] The resulting nucleic acid molecule derived from coryneform bacteria is labeled. Labeling can be carried out according to a method using a fluorescent dye, a method using a radioisotope or the like.

[0170] Specific examples include a labeling method in which psoralen-biotin is crosslinked with RNA extracted from a microorganism and, after hybridization reaction, a fluorescent dye having streptoavidin bound thereto is bound to the biotin moiety (*Nat. Biotechnol.*, *16*: 45-48 (1998)); a labeling method in which a reverse transcription reaction is carried out using RNA extracted from a microorganism as a template and random primers as primers, and dUTP having a fluorescent dye (for example, Cy3, Cy5) (manufactured by Amersham Pharmacia Biotech) is incorporated into cDNA (*Proc. Natl. Acad. Sci. USA*, *96*: 12833-38 (1999)); and the like.

[0171] The labeling specificity can be improved by replacing the random primers by sequences complementary to the 3'-end of ORF (*J. Bacteriol.*, *181*: 6425-40 (1999))

[0172] In the hybridization method, the hybridization and subsequent washing can be carried out by the general method (*Nat. Bioctechnol.*, *14*: 1675-80 (1996), or the like).

[0173] Subsequently, the hybridization intensity is measured depending on the hybridization amount of the nucleic acid molecule used in the labeling. Thus, the mutation point can be identified and the expression amount of the gene can be calculated.

[0174] The hybridization intensity can be measured by visualizing the fluorescent signal, radioactivity, luminescence dose and the like, using a laser confocal microscope, a CCD camera, a radiation imaging device (for example, STORM manufactured by Amersham Pharmacia Biotech), and the like, and then quantifying the thus visualized data.

[0175] A polynucleotide array on a solid support can also be analyzed and quantified using a commercially available apparatus, such as GMS418 Array Scanner (manufactured by Takara Shuzo) or the like.

[0176] The gene expression amount can be analyzed using a commercially available software (for example, ImaGene manufactured by Takara Shuzo; Array Gauge manufactured by Fuji Photo Film; ImageQuant manufactured by Amersham Pharmacia Biotech, or the like).

[0177] A fluctuation in the expression amount of a specific gene can be monitored using a nucleic acid molecule obtained in the time course of culture as the nucleic acid molecule derived from coryneform bacteria. The culture conditions can be optimized by analyzing the fluctuation.

[0178] The expression profile of the microorganism at the total gene level (namely, which genes among a great number of genes encoded by the genome have been expressed and the expression ratio thereof) can be determined using a nucleic acid molecule having the sequences of many genes determined from the full genome sequence of the microorganism. Thus, the expression amount of the genes determined by the full genome sequence can be analyzed and, in its turn, the biological conditions of the microorganism can be recognized as the expression pattern at the full gene level.

(b) Confirmation of the presence of gene homologous to examined gene in coryneform bacteria

[0179] Whether or not a gene homologous to the examined gene, which is present in an organism other than coryneform bacteria, is present in coryneform bacteria can be detected using the polynucleotide array prepared in the above (1).

[0180] This detection can be carried out by a method in which an examined gene which is present in an organism other than coryneform bacteria is used instead of the nucleic acid molecule derived from coryneform bacteria used in the above identification/analysis method of (1).

8. Recording medium storing full genome nucleotide sequence and ORF data and being readable by a computer and methods for using the same

[0181] The term "recording medium or storage device which is readable by a computer" means a recording medium or storage medium which can be directly readout and accessed with a computer. Examples include magnetic recording media, such as a floppy disk, a hard disk, a magnetic tape, and the like; optical recording media, such as CD-ROM, CD-R, CD-RW, DVD-ROM, DVD-RAM, DVD-RW, and the like; electric recording media, such as RAM, ROM, and the like; and hybrids in these categories (for example, magnetic/optical recording media, such as MO and the like).

[0182] Instruments for recording or inputting in or on the recording medium or instruments or devices for reading out the information in the recording medium can be appropriately selected depending on the type of the recording medium

and the access device utilized. Also, various data processing programs, software, comparator and formats are used for recording and utilizing the polynucleotide sequence information or the like, of the present invention in the recording medium. The information can be expressed in the form of a binary file, a text file or an ASCII file formatted with commercially available software, for example. Moreover, software for accessing the sequence information is available and known to one of ordinary skill in the art.

[0183] Examples of the information to be recorded in the above-described medium include the full genome nucleotide sequence information of coryneform bacteria as obtained in the above item 2, the nucleotide sequence information of ORF, the amino acid sequence information encoded by the ORF, and the functional information of polynucleotides coding for the amino acid sequences.

[0184] The recording medium or storage device which is readable by a computer according to the present invention refers to a medium in which the information of the present invention has been recorded. Examples include recording media or storage devices which are readable by a computer storing the nucleotide sequence information represented by SEQ ID NOS:1 to 3501, the amino acid sequence information represented by SEQ ID NOS:3502 to 7001, the functional information of the nucleotide sequences represented by SEQ ID NOS:1 to 3501, the functional information of the amino acid sequences represented by SEQ ID NOS:3502 to 7001, and the information listed in Table 1 below and the like.

9. System based on a computer using the recording medium of the present invention which is readable by a computer

[0185] The term "system based on a computer" as used herein refers a system composed of hardware device(s), software device(s), and data recording device(s) which are used for analyzing the data recorded in the recording medium of the present invention which is readable by a computer.

[0186] The hardware device(s) are, for example, composed of an input unit, a data recording unit, a central processing unit and an output unit collectively or individually.

[0187] By the software device(s), the data recorded in the recording medium of the present invention are searched or analyzed using the recorded data and the hardware device(s) as described herein. Specifically, the software device (s) contain at least one program which acts on or with the system in order to screen, analyze or compare biologically meaningful structures or information from the nucleotide sequences, amino acid sequences and the like recorded in the recording medium according to the present invention.

[0188] Examples of the software device(s) for identifying ORF and EMF domains include GeneMark (*Nuc. Acids. Res., 22*: 4756-67 (1994)), GeneHacker (*Protein, Nucleic Acid and Enzyme, 42*: 3001-07 (1997)), Glimmer (The Institute of Genomic Research: *Nuc. Acids. Res., 26*: 544-548 (1998)) and the like. In the process of using such a software device, the default (initial setting) parameters are usually used, although the parameters can be changed, if necessary, in a manner known to one of ordinary skill in the art.

[0189] Examples of the software device(s) for identifying a genome domain or a polypeptide domain analogous to the target sequence or the target structural motif (homology searching) include FASTA, BLAST, Smith-Waterman, GenetyxMac (manufactured by Software Development), GCG Package (manufactured by Genetic Computer Group), GenCore (manufactured by Compugen), and the like. In the process of using such a software device, the default (initial setting) parameters are usually used, although the parameters can be changed, if necessary, in a manner known to one of ordinary skill in the art.

[0190] Such a recording medium storing the full genome sequence data is useful in preparing a polynucleotide array by which the expression amount of a gene encoded by the genome DNA of coryneform bacteria and the expression profile at the total gene level of the microorganism, namely, which genes among many genes encoded by the genome have been expressed and the expression ratio thereof, can be determined.

[0191] The data recording device(s) provided by the present invention are, for example, memory device(s) for recording the data recorded in the recording medium of the present invention and target sequence or target structural motif data, or the like, and a memory accessing device(s) for accessing the same.

[0192] Namely, the system based on a computer according to the present invention comprises the following:

(i) a user input device that inputs the information stored in the recording medium of the present invention, and target sequence or target structure motif information;
(ii) a data storage device for at least temporarily storing the input information;
(iii) a comparator that compares the information stored in the recording medium of the present invention with the target sequence or target structure motif information, recorded by the data storing device of (ii) for screening and analyzing nucleotide sequence information which is coincident with or analogous to the target sequence or target structure motif information; and
(iv) an output device that shows a screening or analyzing result obtained by the comparator.

[0193] This system is usable in the methods in items 2 to 5 as described above for searching and analyzing the ORF and EMF domains, target sequence, target structural motif, etc. of a coryneform bacterium, searching homologs, searching and analyzing isozymes, determining the biosynthesis pathway and the signal transmission pathway, and identifying spots which have been found in the proteome analysis. The term "homologs" as used herein incluces both of orthologs and paralogs

10. Production of polypeptide using ORF derived from coryneform bacteria

[0194] The polypeptide of the present invention can be produced using a polynucleotide comprising the ORF obtained in the above item 2. Specifically, the polypeptide of the present invention can be produced by expressing the polynucleotide of the present invention or a fragment thereof in a host cell, using the method described in *Molecular Cloning*, 2nd ed., *Current Protocols in Molecular Biology*, and the like, for example, according to the following method.

[0195] A DNA fragment having a suitable length containing a part encoding the polypeptide is prepared from the full length ORF sequence, if necessary.

[0196] Also, DNA in which nucleotides in a nucleotide sequence at a part encoding the polypeptide of the present invention are replaced to give a codon suitable for expression of the host cell, if necessary. The DNA is useful for efficiently producing the polypeptide of the present invention.

[0197] A recombinant vector is prepared by inserting the DNA fragment into the downstream of a promoter in a suitable expression vector.

[0198] The recombinant vector is introduced to a host cell suitable for the expression vector.

[0199] Any of bacteria, yeasts, animal cells, insect cells, plant cells, and the like can be used as the host cell so long as it can be expressed in the gene of interest.

[0200] Examples of the expression vector include those which can replicate autonomously in the above-described host cell or can be integrated into chromosome and have a promoter at such a position that the DNA encoding the polypeptide of the present invention can be transcribed.

[0201] When a procaryote cell, such as a bacterium or the like, is used as the host cell, it is preferred that the recombinant vector containing the DNA encoding the polypeptide of the present invention can replicate autonomously in the bacterium and is a recombinant vector constituted by, at least a promoter, a ribosome binding sequence, the DNA of the present invention and a transcription termination sequence. A promoter controlling gene can also be contained therewith in operable combination.

[0202] Examples of the expression vectors include a vector plasmid which is replicable in *Corynebacterium glutamicum*, such as pCG1 (Japanese Published Unexamined Patent Application No. 134500/82), pCG2 (Japanese Published Unexamined Patent Application No. 35197/83), pCG4 (Japanese Published Unexamined Patent Application No. 183799/82), pCG11 (Japanese Published Unexamined Patent Application No. 134500/82), pCG116, pCE54 and pCB101 (Japanese Published Unexamined Patent Application No. 105999/83), pCE51, pCE52 and pCE53 (*Mol. Gen. Genet., 196*: 175-178 (1984)), and the like; a vector plasmid which is replicable in *Escherichia coli*, such as pET3 and pET11 (manufactured by Stratagene), pBAD, pThioHis and pTrcHis (manufactured by Invitrogen), pKK223-3 and pGEX2T (manufactured by Amersham Pharmacia Biotech), and the like; and pBTrp2, pBTac1 and pBTac2 (manufactured by Boehringer Mannheim Co.), pSE280 (manufactured by Invitrogen), pGEMEX-1 (manufactured by Promega), pQE-8 (manufactured by QIAGEN), pKYP10 (Japanese Published Unexamined Patent Application No. 110600/83), pKYP200 (*Agric. Biol. Chem., 48*: 669 (1984)), pLSA1 (*Agric. Biol. Chem., 53*: 277 (1989)), pGEL1 (*Proc. Natl. Acad. Sci. USA, 82*: 4306 (1985)), pBluescript II SK(-) (manufactured by Stratagene), pTrs30 (prepared from *Escherichia coli* JM109/pTrS30 (FERM BP-5407)), pTrs32 (prepared from *Escherichia coli* JM109/pTrS32 (FERM BP-5408)), pGHA2 (prepared from *Escherichia coli* IGHA2 (FERM B-400), Japanese Published Unexamined Patent Application No. 221091/85), pGKA2 (prepared from *Escherichia coli* IGKA2 (FERM BP-6798), Japanese Published Unexamined Patent Application No. 221091/85), pTerm2 (U.S. Patents 4,686,191, 4,939,094 and 5,160,735), pSupex, pUB110, pTP5, pC194 and pEG400 (*J. Bacteriol., 172*: 2392 (1990)), pGEX (manufactured by Pharmacia), pET system (manufactured by Novagen), and the like.

[0203] Any promoter can be used so long as it can function in the host cell. Examples include promoters derived from *Escherichia coli*, phage and the like, such as *trp* promoter (P_{trp}), *lac* promoter, P_L promoter, P_R promoter, T7 promoter and the like. Also, artificially designed and modified promoters, such as a promoter in which two P*trp* are linked in series (P_{trp} x 2), *tac* promoter, *lac*T7 promoter *let*I promoter and the like, can be used.

[0204] It is preferred to use a plasmid in which the space between Shine-Dalgarno sequence which is the ribosome binding sequence and the initiation codon is adjusted to an appropriate distance (for example 6 to 18 nucleotides).

[0205] The transcription termination sequence is not always necessary for the expression of the DNA of the present invention. However, it is preferred to arrange the transcription terminating sequence at just downstream of the structural gene.

[0206] One of ordinary skill in the art will appreciate that the codons of the above-described elements may be opti-

mized, in a known manner, depending on the host cells and environmental conditions utilized.

[0207] Examples of the host cell include microorganisms belonging to the genus *Escherichia*, the genus *Serratia*, the genus *Bacillus*, the genus *Brevibacterium*, the genus *Corynebacterium*, the genus *Microbacterium*, the genus *Pseudomonas*, and the like. Specific examples include *Escherichia coli* XL1-Blue, *Escherichia coli* XL2-Blue, *Escherichia coli* DH1, *Escherichia coli* MC1000, *Escherichia coli* KY3276, *Escherichia coli* W1485, *Escherichia coli* JM109, *Escherichia coli* HB101, *Escherichia coli* No. 49, *Escherichia coli* W3110, *Escherichia coli* NY49, *Escherichia coli* GI698, *Escherichia coli* TB1, *Serratia ficaria*, *Serratia fonticola*, *Serratia liquefaciens*, *Serratia marcescens*, *Bacillus subtilis*, *Bacillus amyloliquefaciens*, *Corynebacterium ammonia genes*, *Brevibacterium immariophilum* ATCC 14068, *Brevibacterium saccharolyticum* ATCC 14066, *Corynebacterium glutamicum* ATCC 13032, *Corynebacterium* glutamicum ATCC 13869, *Corynebacterium glutamicum* ATCC 14067 (prior genus and species: *Brevibacterium flavum*), *Corynebacterium glutamicum* ATCC 13869 (prior genus and species *Brevibacterium lactofermentum*, or *Corynebacterium lactofermentum*), *Corynebacterium acetoacidophilum* ATCC 13870, *Corynebacterium thermoaminogenes* FERM 9244, *Microbacterium ammoniaphilum* ATCC 15354, *Pseudomonas putida*, *Pseudomonas* sp. D-0110, and the like.

[0208] When *Corynebacterium glutamicum* or an analogous microorganism is used as a host, an EMF necessary for expressing the polypeptide is not always contained in the vector so long as the polynucleotide of the present invention contains an EMF. When the EMF is not contained in the polynucleotide, it is necessary to prepare the EMF separately and ligate it so as to be in operable combination. Also, when a higher expression amount or specific expression regulation is necessary, it is necessary to ligate the EMF corresponding thereto so as to put the EMF in operable combination with the polynucleotide. Examples of using an externally ligated EMF are disclosed in *Microbiology, 142*: 1297-1309 (1996).

[0209] With regard to the method for the introduction of the recombinant vector, any method for introducing DNA into the above-described host cells, such as a method in which a calcium ion is used (*Proc. Natl. Acad. Sci. USA, 69*: 2110 (1972)), a protoplast method (Japanese Published Unexamined Patent Application No. 2483942/88), the methods described in *Gene, 17*: 107 (1982) and *Molecular & General Genetics, 168*: 111 (1979) and the like, can be used.

[0210] When yeast is used as the host cell, examples of the expression vector include pYES2 (manufactured by Invitrogen), YEp13 (ATCC 37115), YEp24 (ATCC 37051), YCp50 (ATCC 37419), pHS19, pHS15, and the like.

[0211] Any promoter can be used so long as it can be expressed in yeast. Examples include a promoter of a gene in the glycolytic pathway, such as hexose kinase and the like, PHO5 promoter, PGK promoter, GAP promoter, ADH promoter, gal 1 promoter, gal 10 promoter, a heat shock protein promoter, MF al promoter, CUP 1 promoter, and the like.

[0212] Examples of the host cell include microorganisms belonging to the genus *Saccharomyces*, the genus *Schizosaccharomyces*, the genus *Kluyveromyces*, the genus *Trichosporon*, the genus *Schwanniomyces*, the genus *Pichia*, the genus *Candida* and the like. Specific examples include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces lactis*, *Trichosporon pullulans*, *Schwanniomyces alluvius*, *Candida utilis* and the like.

[0213] With regard to the method for the introduction of the recombinant vector, any method for introducing DNA into yeast, such as an electroporation method (*Methods. Enzymol., 194*: 182 (1990)), a spheroplast method (*Proc. Natl. Acad. Sci. USA, 75*: 1929 (1978)), a lithium acetate method (*J. Bacteriol., 153*: 163 (1983)), a method described in *Proc. Natl. Acad. Sci. USA, 75*: 1929 (1978) and the like, can be used.

[0214] When animal cells are used as the host cells, examples of the expression vector include pcDNA3.1, pSinRep5 and pCEP4 (manufactured by Invitorogen), pRev-Tre (manufactured by Clontech), pAxCAwt (manufactured by Takara Shuzo), pcDNAI and pcDM8 (manufactured by Funakoshi), pAGE107 (Japanese Published Unexamined Patent Application No. 22979/91; *Cytotechnology, 3*:133 (1990)), pAS3-3 (Japanese Published Unexamined Patent Application No. 227075/90), pcDM8 (*Nature, 329*: 840 (1987)), pcDNAI/Amp (manufactured by Invitrogen), pREP4 (manufactured by Invitrogen), pAGE103 (*J. Biochem., 101*: 1307 (1987)), pAGE210, and the like.

[0215] Any promoter can be used so long as it can function in animal cells. Examples include a promoter of IE (immediate early) gene of cytomegalovirus (CMV), an early promoter of SV40, a promoter of retrovirus, a metallothionein promoter, a heat shock promoter, SRα promoter, and the like. Also, the enhancer of the IE gene of human CMV can be used together with the promoter.

[0216] Examples of the host cell include human Namalwa cell, monkey COS cell, Chinese hamster CHO cell, HST5637 (Japanese Published Unexamined Patent Application No. 299/88), and the like.

[0217] The method for introduction of the recombinant vector into animal cells is not particularly limited, so long as it is the general method for introducing DNA into animal cells, such as an electroporation method (*Cytotechnology, 3*: 133 (1990)), a calcium phosphate method (Japanese Published Unexamined Patent Application No. 227075/90), a lipofection method (*Proc. Natl. Acad. Sci. USA, 84*: 7413 (1987)), the method described in *Virology, 52*: 456 (1973), and the like.

[0218] When insect cells are used as the host cells, the polypeptide can be expressed, for example, by the method described in *Bacurovirus Expression Vectors, A Laboratory Manual*, W.H. Freeman and Company, New York (1992), *Bio/Technology, 6*: 47 (1988), or the like.

[0219] Specifically, a recombinant gene transfer vector and bacurovirus are simultaneously inserted into insect cells

to obtain a recombinant virus in an insect cell culture supernatant, and then the insect cells are infected with the resulting recombinant virus to express the polypeptide.

[0220] Examples of the gene introducing vector used in the method include pBlueBac4.5, pVL1392, pVL1393 and pBlueBacII (manufactured by Invitrogen), and the like.

[0221] Examples of the baculovirus include Autographa californica nuclear polyhedrosis virus with which insects of the family *Barathra* are infected, and the like.

[0222] Examples of the insect cells include *Spodoptera frugiperda* oocytes Sf9 and Sf21 (*Baculovirus Expression Vectors, A Laboratory Manual*, W.H. Freeman and Company, New York (1992)), *Trichoplusia ni* oocyte High 5 (manufactured by Invitrogen) and the like.

[0223] The method for simultaneously incorporating the above-described recombinant gene transfer vector and the above-described baculovirus for the preparation of the recombinant virus include calcium phosphate method (Japanese Published Unexamined Patent Application No. 227075/90), lipofection method (*Proc. Natl. Acad. Sci. USA, 84*: 7413 (1987)) and the like.

[0224] When plant cells are used as the host cells, examples of expression vector include a Ti plasmid, a tobacco mosaic virus vector, and the like.

[0225] Any promoter can be used so long as it can be expressed in plant cells. Examples include 35S promoter of cauliflower mosaic virus (CaMV), rice actin 1 promoter, and the like.

[0226] Examples of the host cells include plant cells and the like such as tobacco, potato, tomato, carrot, soybean, rape, alfalfa, rice, wheat, barley, and the like.

[0227] The method for introducing the recombinant vector is not particularly limited, so long as it is the general method for introducing DNA into plant cells, such as the *Agrobacterium* method (Japanese Published Unexamined Patent Application No. 140885/84, Japanese Published Unexamined Patent Application No. 70080/85, WO 94/00977), the electroporation method (Japanese Published Unexamined Patent Application No. 251887/85), the particle gun method (Japanese Patents 2606856 and 2517813), and the like.

[0228] The transformant of the present invention includes a transformant containing the polypeptide of the present invention *per se* rather than as a recombinant vector, that is, a transformant containing the polypeptide of the present invention which is integrated into a chromosome of the host, in addition to the transformant containing the above recombinant vector.

[0229] When expressed in yeasts, animal cells, insect cells or plant cells, a glycopolypeptide or glycosylated polypeptide can be obtained.

[0230] The polypeptide can be produced by culturing the thus obtained transformant of the present invention in a culture medium to produce and accumulate the polypeptide of the present invention or any polypeptide expressed under the control of an EMF of the present invention, and recovering the polypeptide from the culture.

[0231] Culturing of the transformant of the present invention in a culture medium is carried out according to the conventional method as used in culturing of the host.

[0232] When the transformant of the present invention is obtained using a prokaryote, such as *Escherichia coli* or the like, or a eukaryote, such as yeast or the like, as the host, the transformant is cultured.

[0233] Any of a natural medium and a synthetic medium can be used, so long as it contains a carbon source, a nitrogen source, an inorganic salt and the like which can be assimilated by the transformant and can perform culturing of the transformant efficiently.

[0234] Examples of the carbon source include those which can be assimilated by the transformant, such as carbohydrates (for example, glucose, fructose, sucrose, molasses containing them, starch, starch hydrolysate, and the like), organic acids (for example, acetic acid, propionic acid, and the like), and alcohols (for example, ethanol, propanol, and the like).

[0235] Examples of the nitrogen source include ammonia, various ammonium salts of inorganic acids or organic acids (for example, ammonium chloride, ammonium sulfate, ammonium acetate, ammonium phosphate, and the like), other nitrogen-containing compounds, peptone, meat extract, yeast extract, corn steep liquor, casein hydrolysate, soybean meal and soybean meal hydrolysate, various fermented cells and hydrolysates thereof, and the like.

[0236] Examples of inorganic salt include potassium dihydrogen phosphate, dipotassium hydrogen phosphate, magnesium phosphate, magnesium sulfate, sodium chloride, ferrous sulfate, manganese sulfate, copper sulfate, calcium carbonate, and the like.

[0237] The culturing is carried out under aerobic conditions by shaking culture, submerged-aeration stirring culture or the like. The culturing temperature is preferably from 15 to 40°C, and the culturing time is generally from 16 hours to 7 days. The pH of the medium is preferably maintained at 3.0 to 9.0 during the culturing. The pH can be adjusted using an inorganic or organic acid, an alkali solution, urea, calcium carbonate, ammonia, or the like.

[0238] Also, antibiotics, such as ampicillin, tetracycline, and the like, can be added to the medium during the culturing, if necessary.

[0239] When a microorganism transformed with a recombinant vector containing an inducible promoter is cultured,

an inducer can be added to the medium, if necessary

[0240] For example, isopropyl-β-D-thiogalactopyranoside (IPTG) or the like can be added to the medium when a microorganism transformed with a recombinant vector containing *lac* promoter is cultured, or indoleacrylic acid (IAA) or the like can by added thereto when a microorganism transformed with an expression vector containing *trp* promoter is cultured.

[0241] Examples of the medium used in culturing a transformant obtained using animal cells as the host cells include RPMI 1640 medium (*The Journal of the American Medical Association, 199*: 519 (1967)), Eagle's MEM medium (*Science, 122*: 501 (1952)), Dulbecco's modified MEM medium (*Virology, 8*: 396 (1959)), 199 Medium (*Proceeding of the Society for the Biological Medicine, 73*:1 (1950)), the above-described media to which fetal calf serum has been added, and the like.

[0242] The culturing is carried out generally at a pH of 6 to 8 and a temperature of 30 to 40°C in the presence of 5% CO_2 for 1 to 7 days.

[0243] Also, if necessary, antibiotics, such as kanamycin, penicillin, and the like, can be added to the medium during the culturing.

[0244] Examples of the medium used in culturing a transformant obtained using insect cells as the host cells include TNM-FH medium (manufactured by Pharmingen), Sf-900 II SFM (manufactured by Life Technologies), ExCell 400 and ExCell 405 (manufactured by JRH Biosciences), Grace's Insect Medium (*Nature, 195*: 788 (1962)), and the like.

[0245] The culturing is carried out generally at a pH of 6 to 7 and a temperature of 25 to 30°C for 1 to 5 days.

[0246] Additionally, antibiotics, such as gentamicin and the like, can be added to the medium during the culturing, if necessary.

[0247] A transformant obtained by using a plant cell as the host cell can be used as the cell or after differentiating to a plant cell or organ. Examples of the medium used in the culturing of the transformant include Murashige and Skoog (MS) medium, White medium, media to which a plant hormone, such as auxin, cytokinine, or the like has been added, and the like.

[0248] The culturing is carried out generally at a pH of 5 to 9 and a temperature of 20 to 40°C for 3 to 60 days.

[0249] Also, antibiotics, such as kanamycin, hygromycin and the like, can be added to the medium during the culturing, if necessary.

[0250] As described above, the polypeptide can be produced by culturing a transformant derived from a microorganism, animal cell or plant cell containing a recombinant vector to which a DNA encoding the polypeptide of the present invention has been inserted according to the general culturing method to produce and accumulate the polypeptide, and recovering the polypeptide from the culture.

[0251] The process of gene expression may include secretion of the encoded protein production or fusion protein expression and the like in accordance with the methods described in *Molecular Cloning*, 2nd ed., in addition to direct expression.

[0252] The method for producing the polypeptide of the present invention includes a method of intracellular expression in a host cell, a method of extracellular secretion from a host cell, or a method of production on a host cell membrane outer envelope. The method can be selected by changing the host cell employed or the structure of the polypeptide produced.

[0253] When the polypeptide of the present invention is produced in a host cell or on a host cell membrane outer envelope, the polypeptide can be positively secreted extracellularly according to, for example, the method of Paulson *et al.* (*J. Biol. Chem., 264*: *17619* (1989)), the method of Lowe *et al.* (*Proc. Natl. Acad. Sci. USA, 86*: 8227 (1989); *Genes Develop., 4*: 1288 (1990)), and/or the methods described in Japanese Published Unexamined Patent Application No. 336963/93, WO 94/23021, and the like.

[0254] Specifically, the polypeptide of the present invention can be positively secreted extracellularly by expressing it in the form that a signal peptide has been added to the foreground of a polypeptide containing an active site of the polypeptide of the present invention according to the recombinant DNA technique.

[0255] Furthermore, the amount produced can be increased using a gene amplification system, such as by use of a dihydrofolate reductase gene or the like according to the method described in Japanese Published Unexamined Patent Application No. 227075/90.

[0256] Moreover, the polypeptide of the present invention can be produced by a transgenic animal individual (transgenic nonhuman animal) or plant individual (transgenic plant).

[0257] When the transformant is the animal individual or plant individual, the polypeptide of the present invention can be produced by breeding or cultivating it so as to produce and accumulate the polypeptide, and recovering the polypeptide from the animal individual or plant individual.

[0258] Examples of the method for producing the polypeptide of the present invention using the animal individual include a method for producing the polypeptide of the present invention in an animal developed by inserting a gene according to methods known to those of ordinary skill in the art (*American Journal of Clinical Nutrition, 63*: 639S (1996), *American Journal of Clinical Nutrition, 63*: 627S (1996), *Bio/Technology, 9*: 830 (1991)).

[0259] In the animal individual, the polypeptide can be produced by breeding a transgenic nonhuman animal to which the DNA encoding the polypeptide of the present invention has been inserted to produce and accumulate the polypeptide in the animal, and recovering the polypeptide from the animal. Examples of the production and accumulation place in the animal include milk (Japanese Published Unexamined Patent Application No. 309192/88), egg and the like of the animal. Any promoter can be used, so long as it can be expressed in the animal. Suitable examples include an α-casein promoter, a (β-casein promoter, a β-lactoglobulin promoter, a whey acidic protein promoter, and the like, which are specific for mammary glandular cells.

[0260] Examples of the method for producing the polypeptide of the present invention using the plant individual include a method for producing the polypeptide of the present invention by cultivating a transgenic plant to which the DNA encoding the protein of the present invention by a known method (*Tissue Culture, 20* (1994), *Tissue Culture, 21* (1994), *Trends in Biotechnology, 15:* 45 (1997)) to produce and accumulate the polypeptide in the plant, and recovering the polypeptide from the plant.

[0261] The polypeptide according to the present invention can also be obtained by translation *in vitro.*

[0262] The polypeptide of the present invention can be produced by a translation system *in vitro.* There are, for example, two *in vitro* translation methods which may be used, namely, a method using RNA as a template and another method using DNA as a template. The template RNA includes the whole RNA, mRNA, an *in vitro* transcription product, and the like. The template DNA includes a plasmid containing a transcriptional promoter and a target gene integrated therein and downstream of the initiation site, a PCR/RT-PCR product and the like. To select the most suitable system for the *in vitro* translation, the origin of the gene encoding the protein to be synthesized (prokaryotic cell/eucaryotic cell), the type of the template (DNA/RNA), the purpose of using the synthesized protein and the like should be considered. *In vitro* translation kits having various characteristics are commercially available from many companies (Boehringer Mannheim, Promega, Stratagene, or the like), and every kit can be used in producing the polypeptide according to the present invention.

[0263] Transcription/translation of a DNA nucleotide sequence cloned into a plasmid containing a T7 promoter can be carried out using an *in vitro* transcription/translation system *E. coli* T7 S30 Extract System for Circular DNA (manufactured by Promega, catalogue No. L1130). Also, transcription/translation using, as a template, a linear prokaryotic DNA of a supercoil non-sensitive promoter, such as *lac*UV5, *tac*, λPL(con), λPL, or the like, can be carried out using an *in vitro* transcription/translation system *E. coli* S30 Extract System for Linear Templates (manufactured by Promega, catalogue No. L1030). Examples of the linear prokaryotic DNA used as a template include a DNA fragment, a PCR-amplified DNA product, a duplicated oligonucleotide ligation, an *in vitro* transcriptional RNA, a prokaryotic RNA, and the like.

[0264] In addition to the production of the polypeptide according to the present invention, synthesis of a radioactive labeled protein, confirmation of the expression capability of a cloned gene, analysis of the function of transcriptional reaction or translation reaction, and the like can be carried out using this system.

[0265] The polypeptide produced by the transformant of the present invention can be isolated and purified using the general method for isolating and purifying an enzyme. For example, when the polypeptide of the present invention is expressed as a soluble product in the host cells, the cells are collected by centrifugation after cultivation, suspended in an aqueous buffer, and disrupted using an ultrasonicator, a French press, a Manton Gaulin homogenizer, a Dynomill, or the like to obtain a cell-free extract. From the supernatant obtained by centrifuging the cell-free extract, a purified product can be obtained by the general method used for isolating and purifying an enzyme, for example, solvent extraction, salting out using ammonium sulfate or the like, desalting, precipitation using an organic solvent, anion exchange chromatography using a resin, such as diethylaminoethyl (DEAE)-Sepharose, DIAION HPA-75 (manufactured by Mitsubishi Chemical) or the like, cation exchange chromatography using a resin, such as S-Sepharose FF (manufactured by Pharmacia) or the like, hydrophobic chromatography using a resin, such as butyl sepharose, phenyl sepharose or the like, gel filtration using a molecular sieve, affinity chromatography, chromatofocusing, or electrophoresis, such as isoelectronic focusing or the like, alone or in combination thereof.

[0266] When the polypeptide is expressed as an insoluble product in the host cells, the cells are collected in the same manner, disrupted and centrifuged to recover the insoluble product of the polypeptide as the precipitate fraction. Next, the insoluble product of the polypeptide is solubilized with a protein denaturing agent. The solubilized solution is diluted or dialyzed to lower the concentration of the protein denaturing agent in the solution. Thus, the normal configuration of the polypeptide is reconstituted. After the procedure, a purified product of the polypeptide can be obtained by a purification/isolation method similar to the above.

[0267] When the polypeptide of the present invention or its derivative (for example, a polypeptide formed by adding a sugar chain thereto) is secreted out of cells, the polypeptide or its derivative can be collected in the culture supernatant. Namely, the culture supernatant is obtained by treating the culture medium in a treatment similar to the above (for example, centrifugation). Then, a purified product can be obtained from the culture medium using a purification/isolation method similar to the above.

[0268] The polypeptide obtained by the above method is within the scope of the polypeptide of the present invention.

and examples include a polypeptide encoded by a polynucleotide comprising the nucleotide sequence selected from SEQ ID NOS:2 to 3431, and a polypeptide comprising an amino acid sequence represented by any one of SEQ ID NOS 3502 to 6931.

[0269] Furthermore, a polypeptide comprising an amino acid sequence in which at least one amino acids is deleted, replaced, inserted or added in the amino acid sequence of the polypeptide and having substantially the same activity as that of the polypeptide is included in the scope of the present invention. The term "substantially the same activity as that of the polypeptide" means the same activity represented by the inherent function, enzyme activity or the like possessed by the polypeptide which has not been deleted, replaced, inserted or added. The polypeptide can be obtained using a method for introducing part-specific mutation(s) described in, for example, *Molecular Cloning*, 2nd ed., *Current Protocols in Molecular Biology, Nuc. Acids. Res., 10*: 6487 (1982), *Proc. Natl. Acad. Sci. USA, 79*: 6409 (1982), *Gene, 34*: 315 (1985), *Nuc. Acids. Res., 13*: 4431 (1985), *Proc. Natl. Acad. Sci. USA, 82*: 488 (1985) and the like. For example, the polypeptide can be obtained by introducing mutation(s) to DNA encoding a polypeptide having the amino acid sequence represented by any one of SEQ ID NOS:3502 to 6931. The number of the amino acids which are deleted, replaced, inserted or added is not particularly limited; however, it is usually 1 to the order of tens, preferably 1 to 20, more preferably 1 to 10, and most preferably 1 to 5, amino acids.

[0270] The at least one amino acid deletion, replacement, insertion or addition in the amino acid sequence of the polypeptide of the present invention is used herein to refer to that at least one amino acid is deleted, replaced, inserted or added to at one or plural positions in the amino acid sequence. The deletion, replacement, insertion or addition may be caused in the same amino acid sequence simultaneously. Also, the amino acid residue replaced, inserted or added can be natural or non-natural. Examples of the natural amino acid residue include L-alanine, L-asparagine, L-asparatic acid, L-glutamine, L-glutamic acid, glycine, L-histidine, L-isoleucine, L-leucine, L-lysine, L-methionine, L-phenylalanine, L-proline, L-serine, L-threonine, L-tryptophan, L-tyrosine, L-valine, L-cysteine, and the like.

[0271] Herein, examples of amino acid residues which are replaced with each other are shown below. The amino acid residues in the same group can be replaced with each other.

Group A:

[0272] leucine, isoleucine, norleucine, valine, norvaline, alanine, 2-aminobutanoic acid, methionine O-methylserine, t-butylglycine, t-butylalanine, cyclohexylalanine;

Group B:

[0273] asparatic acid, glutamic acid, isoasparatic acid, isoglutamic acid, 2-aminoadipic acid, 2-aminosuberic acid;

Group C:

[0274] asparagine, glutamine;

Group D:

[0275] lysine, arginine, ornithine, 2,4-diaminobutanoic acid, 2,3-diaminopropionic acid;

Group E:

[0276] proline, 3-hydroxyproline, 4-hydroxyproline;

Group F:

[0277] serine, threonine, homoserine;

Group G:

[0278] phenylalanine, tyrosine.

[0279] Also, in order that the resulting mutant polypeptide has substantially the same activity as that of the polypeptide which has not been mutated, it is preferred that the mutant polypeptide has a homology of 60% or more, preferably 80% or more, and particularly preferably 95% or more, with the polypeptide which has not been mutated, when calculated, for example, using default (initial setting) parameters by a homology searching software, such as BLAST, FASTA, or the like.

[0280] Also the polypeptide of the present invention can be produced by a chemical synthesis method, such as Fmoc (fluorenylmethyloxycarbonyl) method, tBoc (t-butyloxycarbonyl) method, or the like. It can also be synthesized using a peptide synthesizer manufactured by Advanced ChemTech, Perkin-Elmer, Pharmacia, Protein Technology Instrument, Synthecell-Vega, PerSeptive, Shimadzu Corporation, or the like.

[0281] The transformant of the present invention can be used for objects other than the production of the polypeptide of the present invention.

[0282] Specifically, at least one component selected from an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid, and analogues thereof can be produced by culturing the transformant containing the polynucleotide or recombinant vector of the present invention in a medium to produce and accumulate at least one component selected from amino acids, nucleic acids, vitamins, saccharides, organic acids, and analogues thereof, and recovering the same from the medium.

[0283] The biosynthesis pathways, decomposition pathways and regulatory mechanisms of physiologically active substances such as amino acids, nucleic acids, vitamins, saccharides, organic acids and analogues thereof differ from organism to organism. The productivity of such a physiologically active substance can be improved using these differences, specifically by introducing a heterogeneous gene relating to the biosynthesis thereof. For example, the content of lysine, which is one of the essential amino acids, in a plant seed was improved by introducing a synthase gene derived from a bacterium (WO 93/19190). Also, arginine is excessively produced in a culture by introducing an arginine synthase gene derived from *Escherichia coli* (Japanese Examined Patent Publication 23750/93).

[0284] To produce such a physiologically active substance, the transformant according to the present invention can be cultured by the same method as employed in culturing the transformant for producing the polypeptide of the present invention as described above. Also, the physiologically active substance can be recovered from the culture medium in combination with, for example, the ion exchange resin method, the precipitation method and other known methods.

[0285] Examples of methods known to one of ordinary skill in the art include electroporation, calcium transfection, the protoplast method, the method using a phage, and the like, when the host is a bacterium; and microinjection, calcium phosphate transfection, the positively charged lipid-mediated method and the method using a virus, and the like, when the host is a eukaryote (*Molecular Cloning*, 2nd ed.; Spector *et al.*, *Cells/a laboratory manual*, Cold Spring Harbour Laboratory Press, 1998)). Examples of the host include prokaryotes, lower eukaryotes (for example, yeasts), higher eukaryotes (for example, mammals), and cells isolated therefrom. As the state of a recombinant polynucleotide fragment present in the host cells, it can be integrated into the chromosome of the host. Alternatively, it can be integrated into a factor (for example, a plasmid) having an independent replication unit outside the chromosome. These transformants are usable in producing the polypeptides of the present invention encoded by the ORF of the genome of *Corynebacterium glutamicum*, the polynucleotides of the present invention and fragments thereof. Alternatively, they can be used in producing arbitrary polypeptides under the regulation by an EMF of the present invention.

11. Preparation of antibody recognizing the polypeptide of the present invention

[0286] An antibody which recognizes the polypeptide of the present invention, such as a polyclonal antibody, a monoclonal antibody, or the like, can be produced using, as an antigen, a purified product of the polypeptide of the present invention or a partial fragment polypeptide of the polypeptide or a peptide having a partial amino acid sequence of the polypeptide of the present invention.

(1) Production of polyclonal antibody

[0287] A polyclonal antibody can be produced using, as an antigen, a purified product of the polypeptide of the present invention, a partial fragment polypeptide of the polypeptide, or a peptide having a partial amino acid sequence of the polypeptide of the present invention, and immunizing an animal with the same.

[0288] Examples of the animal to be immunized include rabbits, goats, rats, mice, hamsters, chickens and the like.

[0289] A dosage of the antigen is preferably 50 to 100 μg per animal.

[0290] When the peptide is used as the antigen, it is preferably a peptide covalently bonded to a carrier protein, such as keyhole limpet haemocyanin, bovine thyroglobulin, or the like. The peptide used as the antigen can be synthesized by a peptide synthesizer.

[0291] The administration of the antigen is, for example, carried out 3 to 10 times at the intervals of 1 or 2 weeks after the first administration. On the 3rd to 7th day after each administration, a blood sample is collected from the venous plexus of the eyeground, and it is confirmed that the serum reacts with the antigen by the enzyme immunoassay (*Enzyme-linked Immunosorbent Assay (ELISA)*, Igaku Shoin (1976) ; *Antibodies - A Laboratory Manual*, Cold Spring Harbor Laboratory (1988)) or the like.

[0292] Serum is obtained from the immunized non-human mammal with a sufficient antibody titer against the antigen used for the immunization, and the serum is isolated and purified to obtain a polyclonal antibody.

[0293] Examples of the method for the isolation and purification include centrifugation, salting out by 40-50% saturated ammonium sulfate, caprylic acid precipitation (*Antibodies, A Laboratory manual*, Cold Spring Harbor Laboratory (1988)), or chromatography using a DEAE-Sepharose column, an anion exchange column, a protein A- or G-column, a gel filtration column, and the like, alone or in combination thereof, by methods known to those of ordinary skill in the art.

(2) Production of monoclonal antibody

(a) Preparation of antibody-producing cell

[0294] A rat having a serum showing an enough antibody titer against a partial fragment polypeptide of the polypeptide of the present invention used for immunization is used as a supply source of an antibody-producing cell.

[0295] On the 3rd to 7th day after the antigen substance is finally administered the rat showing the antibody titer, the spleen is excised.

[0296] The spleen is cut to pieces in MEM medium (manufactured by Nissui Pharmaceutical), loosened using a pair of forceps, followed by centrifugation at 1,200 rpm for 5 minutes, and the resulting supernatant is discarded.

[0297] The spleen in the precipitated fraction is treated with a Tris-ammonium chloride buffer (pH 7.65) for 1 to 2 minutes to eliminate erythrocytes and washed three times with MEM medium, and the resulting spleen cells are used as antibody-producing cells.

(b) Preparation of myeloma cells

[0298] As myeloma cells, an established cell line obtained from mouse or rat is used. Examples of useful cell lines include those derived from a mouse, such as P3-X63Ag8-U1 (hereinafter referred to as "P3-U1") (*Curr. Topics in Microbiol. Immunol., 81*: 1 (1978)); *Europ. J. Immunol., 6*: 511 (1976)); SP2/O-Agl4 (SP-2) (*Nature, 276*: 269 (1978)); P3-X63-Ag8653 (653) (*J. Immunol., 123*: 1548 (1979)); P3-X63-Ag8 (X63) cell line (*Nature, 256*: 495 (1975)), and the like, which are 8-azaguanine-resistant mouse (BALB/c) myeloma cell lines. These cell lines are subcultured in 8-azaguanine medium (medium in which, to a medium obtained by adding 1.5 mmol/l glutamine, 5×10^{-5} mol/l 2-mercaptoethanol, 10 μg/ml gentamicin and 10% fetal calf serum (FCS) (manufactured by CSL) to RPMI-1640 medium (hereinafter referred to as the "normal medium"), 8-azaguanine is further added at 15 μg/ml) and cultured in the normal medium 3 or 4 days before cell fusion, and 2×10^7 or more of the cells are used for the fusion.

(c) Production of hybridoma

[0299] The antibody-producing cells obtained in (a) and the myeloma cells obtained in (b) are washed with MEM medium or PBS (disodium hydrogen phosphate: 1.83 g, sodium dihydrogen phosphate: 0.21 g, sodium chloride: 7.65 g, distilled water: 1 liter, pH: 7.2) and mixed to give a ratio of antibody-producing cells : myeloma cells = 5 : 1 to 10 : 1, followed by centrifugation at 1,200 rpm for 5 minutes, and the supernatant is discarded.

[0300] The cells in the resulting precipitated fraction were thoroughly loosened, 0.2 to 1 ml of a mixed solution of 2 g of polyethylene glycol-1000 (PEG-1000), 2 ml of MEM medium and 0.7 ml of dimethylsulfoxide (DMSO) per 10^8 antibody-producing cells is added to the cells under stirring at 37°C and then 1 to 2 ml of MEM medium is further added thereto several times at 1 to 2 minute intervals.

[0301] After the addition MEM medium is added to give a total amount of 50 ml. The resulting prepared solution is centrifuged at 900 rpm for 5 minutes, and then the supernatant is discarded. The cells in the resulting precipitated fraction were gently loosened and then gently suspended in 100 ml of HAT medium (the normal medium to which 10^{-4} mol/l hypoxanthine, $1.5 \cdot 10^{-5}$ mol/l thymidine and 4×10^{-7} mol/l aminopterin have been added) by repeated drawing up into and discharging from a measuring pipette.

[0302] The suspension is poured into a 96 well culture plate at 100 μl/well and cultured at 37°C for 7 to 14 days in a 5% CO_2 incubator.

[0303] After culturing, a part of the culture supernatant is recovered, and a hybridoma which specifically reacts with a partial fragment polypeptide of the polypeptide of the present invention is selected according to the enzyme immunoassay described in *Antibodies, A Laboratory manual*, Cold Spring Harbor Laboratory, Chapter 14 (1998) and the like.

[0304] A specific example of the enzyme immunoassay is described below.

[0305] The partial fragment polypeptide of the polypeptide of the present invention used as the antigen in the immunization is spread on a suitable plate, is allowed to react with a hybridoma culturing supernatant or a purified antibody obtained in (d) described below as a first antibody, and is further allowed to react with an anti-rat or anti-mouse immunoglobulin antibody labeled with an enzyme, a chemical luminous substance, a radioactive substance or the like as a second antibody for reaction suitable for the labeled substance. A hybridoma which specifically reacts with the polypeptide of the present invention is selected as a hybridoma capable of producing a monoclonal antibody of the present

invention

[0306] Cloning is repeated using the hybridoma twice by limiting dilution analysis (HT medium (a medium in which aminopterin has been removed from HAT medium) is firstly used, and the normal medium is secondly used), and a hybridoma which is stable and contains a sufficient amount of antibody titer is selected as a hybridoma capable of producing a monoclonal antibody of the present invention.

(d) Preparation of monoclonal antibody

[0307] The monoclonal antibody-producing hybridoma cells obtained in (c) are injected intraperitoneally into 8- to 10-week-old mice or nude mice treated with pristane (intraperitoneal administration of 0.5 ml of 2,6,10,14-tetramethylpentadecane (pristane), followed by 2 weeks of feeding) at $5 \cdot 10^6$ to $20 \cdot 10^6$ cells/animal. The hybridoma causes ascites tumor in 10 to 21 days.

[0308] The ascitic fluid is collected from the mice or nude mice, and centrifuged to remove solid contents at 3000 rpm for 5 minutes.

[0309] A monoclonal antibody can be purified and isolated from the resulting supernatant according to the method similar to that used in the polyclonal antibody.

[0310] The subclass of the antibody can be determined using a mouse monoclonal antibody typing kit or a rat monoclonal antibody typing kit. The polypeptide amount can be determined by the Lowry method or by calculation based on the absorbance at 280 nm.

[0311] The antibody obtained in the above is within the scope of the antibody of the present invention.

[0312] The antibody can be used for the general assay using an antibody, such as a radioactive material labeled immunoassay (RIA), competitive binding assay, an immunotissue chemical staining method (ABC method, CSA method, *etc.*), immunoprecipitation, Western blotting, ELISA assay, and the like (*An introduction to Radioimmunoassay and Related Techniques*, Elsevier Science (1986); *Techniques in Immunocytochemistry*, Academic Press, Vol. 1 (1982), Vol. 2 (1983) & Vol. 3 (1985); *Practice and Theory of Enzyme Immunoassays*, Elsevier Science (1985); *Enzyme-linked Immunosorbent Assay (ELISA)*, Igaku Shoin (1976); *Antibodies - A Laboratory Manual*, Cold Spring Harbor laboratory (1988); *Monoclonal Antibody Experiment Manual*, Kodansha Scientific (1987); *Second Series Biochemical Experiment Course*, Vol. 5, Immunobiochemistry Research Method, Tokyo Kagaku Dojin (1986))

[0313] The antibody of the present invention can be used as it is or after being labeled with a label.

[0314] Examples of the label include radioisotope, an affinity label (e.g., biotin, avidin, or the like), an enzyme label (e.g., horseradish peroxidase, alkaline phosphatase, or the like), a fluorescence label (e.g., FITC, rhodamine, or the like), a label using a rhodamine atom. (*J. Histochem. Cytochem., 18*: 315 (1970); *Meth. Enzym., 62*: 308 (1979); *Immunol., 109*: 129 (1972); *J. Immunol., Meth., 13*: 215 (1979)), and the like.

[0315] Expression of the polypeptide of the present invention, fluctuation of the expression, the presence or absence of structural change of the polypeptide, and the presence or absence in an organism other than coryneform bacteria of a polypeptide corresponding to the polypeptide can be analyzed using the antibody or the labeled antibody by the above assay, or a polypeptide array or proteome analysis described below.

[0316] Furthermore, the polypeptide recognized by the antibody can be purified by immunoaffinity chromatography using the antibody of the present invention.

12. Production and use of polypeptide array

(1) Production of polypeptide array

[0317] A polypeptide array can be produced using the polypeptide of the present invention obtained in the above item 10 or the antibody of the present invention obtained in the above item 11.

[0318] The polypeptide array of the present invention includes protein chips, and comprises a solid support and the polypeptide or antibody of the present invention adhered to the surface of the solid support.

[0319] Examples of the solid support include plastic such as polycarbonate or the like; an acrylic resin, such as polyacrylamide or the like; complex carbohydrates, such as agarose, sepharose, or the like; silica; a silica-based material, carbon, a metal, inorganic glass, latex beads, and the like.

[0320] The polypeptides or antibodies according to the present invention can be adhered to the surface of the solid support according to the method described in *Biotechniques, 27*: 1258-61 (1999); *Molecular Medicine Today, 5*: 326-7 (1999); *Handbook of Experimental Immunology*, 4th edition, Blackwell Scientific Publications, Chapter 10 (1986); *Meth. Enzym., 34* (1974); *Advances in Experimental Medicine and Biology, 42* (1974); U.S. Patent 4,681,870; U.S. Patent 4,282,287; U.S. Patent 4,762,881, or the like.

[0321] The analysis described herein can be efficiently performed by adhering the polypeptide or antibody of the present invention to the solid support at a high density, though a high fixation density is not always necessary.

(2) Use of polypeptide array

[0322] A polypeptide or a compound capable of binding to and interacting with the polypeptides of the present invention adhered to the array can be identified using the polypeptide array to which the polypeptides of the present invention have been adhered thereto as described in the above (1).

[0323] Specifically, a polypeptide or a compound capable of binding to and interacting with the polypeptides of the present invention can be identified by subjecting the polypeptides of the present invention to the following steps (i) to (iv):

(i) preparing a polypeptide array having the polypeptide of the present invention adhered thereto by the method of the above (1);
(ii) incubating the polypeptide immobilized on the polypeptide array together with at least one of a second polypeptide or compound;
(iii) detecting any complex formed between the at least one of a second polypeptide or compound and the polypeptide immobilized on the array using, for example, a label bound to the at least one of a second polypeptide or compound, or a secondary label which specifically binds to the complex or to a component of the complex after unbound material has been removed; and
(iv) analyzing the detection data.

[0324] Specific examples of the polypeptide array to which the polypeptide of the present invention has been adhered include a polypeptide array containing a solid support to which at least one of a polypeptide containing an amino acid sequence selected from SEQ ID NOS:3502 to 7001, a polypeptide containing an amino acid sequence in which at least one amino acids is deleted, replaced, inserted or added in the amino acid sequence of the polypeptide and having substantially the same activity as that of the polypeptide, a polypeptide containing an amino acid sequence having a homology of 60% or more with the amino acid sequences of the polypeptide and having substantially the same activity as that of the polypeptides, a partial fragment polypeptide, and a peptide comprising an amino acid sequence of a part of a polypeptide.

[0325] The amount of production of a polypeptide derived from coryneform bacteria can be analyzed using a polypeptide array to which the antibody of the present invention has been adhered in the above (1).

[0326] Specifically, the expression amount of a gene derived from a mutant of coryneform bacteria can be analyzed by subjecting the gene to the following steps (i) to (iv):

(i) preparing a polypeptide array by the method of the above (1);
(ii) incubating the polypeptide array (the first antibody) together with a polypeptide derived from a mutant of coryneform bacteria;
(iii) detecting the polypeptide bound to the polypeptide immobilized on the array using a labeled second antibody of the present invention; and
(iv) analyzing the detection data.

[0327] Specific examples of the polypeptide array to which the antibody of the present invention is adhered include a polypeptide array comprising a solid support to which at least one of an antibody which recognizes a polypeptide comprising an amino acid sequence selected from SEQ ID NOS:3502 to 7001, a polypeptide comprising an amino acid sequence in which at least one amino acids is deleted, replaced, inserted or added in the amino acid sequence of the polypeptide and having substantially the same activity as that of the polypeptide, a polypeptide comprising an amino acid sequence having a homology of 60% or more with the amino acid sequences of the polypeptide and having substantially the same activity as that of the polypeptides, a partial fragment polypeptide, or a peptide comprising an amino acid sequence of a part of a polypeptide.

[0328] A fluctuation in an expression amount of a specific polypeptide can be monitored using a polypeptide obtained in the time course of culture as the polypeptide derived from coryneform bacteria. The culturing conditions can be optimized by analyzing the fluctuation.

[0329] When a polypeptide derived from a mutant of coryneform bacteria is used, a mutated polypeptide can be detected.

13. Identification of useful mutation in mutant by proteome analysis

[0330] Usually, the proteome is used herein to refer to a method wherein a polypeptide is separated by twodimensional electrophoresis and the separated polypeptide is digested with an enzyme, followed by identification of the polypeptide using a mass spectrometer (MS) and searching a data base.

[0331] The two dimensional electrophoresis means an electrophoretic method which is performed by combining two

electrophoretic procedures having different principles. For example, polypeptides are separated depending on molecular weight in the primary electrophoresis. Next, the gel is rotated by 90° or 180° and the secondary electrophoresis is carried out depending on isoelectric point. Thus, various separation patterns can be achieved (JIS K 3600 2474).

[0332] In searching the data base, the amino acid sequence information of the polypeptides of the present invention and the recording medium of the present invention provide for in the above items 2 and 8 can be used.

[0333] The proteome analysis of a coryneform bacterium and its mutant makes it possible to identify a polypeptide showing a fluctuation therebetween.

[0334] The proteome analysis of a wild type strain of coryneform bacteria and a production strain showing an improved productivity of a target product makes it possible to efficiently identify a mutation protein which is useful in breeding for improving the productivity of a target product or a protein of which expression amount is fluctuated.

[0335] Specifically, a wild type strain of coryneform bacteria and a lysine-producing strain thereof are each subjected to the proteome analysis. Then, a spot increased in the lysine-producing strain, compared with the wild type strain, is found and a data base is searched so that a polypeptide showing an increase in yield in accordance with an increase in the lysine productivity can be identified. For example, as a result of the proteome analysis on a wild type strain and a lysine-producing strain, the productivity of the catalase having the amino acid sequence represented by SEQ ID NO: 3785 is increased in the lysine-producing mutant.

[0336] As a result that a protein having a high expression level is identified by proteome analysis using the nucleotide sequence information and the amino acid sequence information, of the genome of the coryneform bacteria of the present invention, and a recording medium storing the sequences, the nucleotide sequence of the gene encoding this protein and the nucleotide sequence in the upstream thereof can be searched at the same time, and thus, a nucleotide sequence having a high expression promoter can be efficiently selected.

[0337] In the proteome analysis, a spot on the two-dimentional electrophoresis gel showing a fluctuation is sometimes derived from a modified protein. However, the modified protein can be efficiently identified using the recording medium storing the nucleotide sequence information, the amino acid sequence information, of the genome of coryneform bacteria, and the recording medium storing the sequences, according to the present invention.

[0338] Moreover, a useful mutation point in a useful mutant can be easily specified by searching a nucleotide sequence (nucleotide sequence of promoters, ORF, or the like) relating to the thus identified protein using a recording medium storing the nucleotide sequence information and the amino acid sequence information, of the genome of coryneform bacteria of the present invention, and a recording medium storing the sequences and using a primer designed on the basis of the detected nucleotide sequence. As a result that the useful mutation point is specified, an industrially useful mutant having the useful mutation or other useful mutation derived therefrom can be easily bred.

[0339] The present invention will be explained in detail below based on Examples. However, the present invention is not limited thereto.

Example 1

Determination of the full nucleotide sequence of genome of *Corynebacterium glutamicum*

[0340] The full nucleotide sequence of the genome of *Corynebacterium glutamicum* was determined based on the whole genome shotgun method (*Science, 269*: 496-512 (1995)). In this method, a genome library was prepared and the terminal sequences were determined at random. Subsequently, these sequences were ligated on a computer to cover the full genome. Specifically, the following procedure was carried out.

(1) Preparation of genome DNA of *Corynebacterium glutamicum* ATCC 13032

[0341] *Corynebacterium glutamicum* ATCC 13032 was cultured in BY medium (7 g/l meat extract, 10 g/l peptone, 3 g/l sodium chloride, 5 g/l yeast extract, pH 7.2) containing 1% of glycine at 30°C overnight and the cells were collected by centrifugation. After washing with STE buffer (10.3% sucrose, 25 mmol/l Tris hydrochloride, 25 mmol/l EDTA, pH 8.0), the cells were suspended in 10 ml of STE buffer containing 10 mg/ml lysozyme, followed by gently shaking at 37°C for 1 hour. Then, 2 ml of 10% SDS was added thereto to lyse the cells, and the resultant mixture was maintained at 65°C for 10 minutes and then cooled to room temperature. Then, 10 ml of Tris-neutralized phenol was added thereto, followed by gently shaking at room temperature for 30 minutes and centrifugation (15,000 × g, 20 minutes, 20°C). The aqueous layer was separated and subjected to extraction with phenol/chloroform and extraction with chloroform (twice) in the same manner. To the aqueous layer, 3 mol/l sodium acetate solution (pH 5.2) and isopropanol were added at 1/10 times volume and twice volume, respectively, followed by gently stirring to precipitate the genome DNA. The genome DNA was dissolved again in 3 ml of TE buffer (10 mmol/l Tris hydrochloride, 1 mmol/l EDTA, pH 8.0) containing 0.02 mg/ml of RNase and maintained at 37°C for 45 minutes. The extractions with phenol, phenol/chloroform and chloroform were carried out successively in the same manner as the above. The genome DNA was subjected to iso-

propanol precipitation. The thus formed genome DNA precipitate was washed with 70% ethanol three times, followed by air-drying, and dissolved in 1.25 ml of TE buffer to give a genome DNA solution (concentration: 0.1 mg/ml).

(2) Construction of a shotgun library

[0342] TE buffer was added to 0.01 mg of the thus prepared genome DNA of *Corynebacterium glutamicum* ATCC 13032 to give a total volume of 0.4 ml, and the mixture was treated with a sonicator (Yamato Powersonic Model 150) at an output of 20 continuously for 5 seconds to obtain fragments of 1 to 10 kb. The genome fragments were blunt-ended using a DNA blunting kit (manufactured by Takara Shuzo) and then fractionated by 6% polyacrylamide gel electrophoresis. Genome fragments of 1 to 2 kb were cut out from the gel, and 0.3 ml MG elution buffer (0.5 mol/l ammonium acetate, 10 mmol/l magnesium acetate, 1 mmol/l EDTA, 0.1% SDS) was added thereto, followed by shaking at 37°C overnight to elute DNA. The DNA eluate was treated with phenol/chloroform, and then precipitated with ethanol to obtain a genome library insert. The total insert and 500 ng of pUC18 *Sma*I/BAP (manufactured by Amersham Pharmacia Biotech) were ligated at 16°C for 40 hours.

[0343] The ligation product was precipitated with ethanol and dissolved in 0.01 ml of TE buffer. The ligation solution (0.001 ml) was introduced into 0.04 ml of *E. coli* ELECTRO MAX DH10B (manufactured by Life Technologies) by the electroporation under conditions according to the manufacture's instructions. The mixture was spread on LB plate medium (LB medium (10 g/l bactotrypton, 5 g/l yeast extract, 10 g/l sodium chloride, pH 7.0) containing 1.6% of agar) containing 0.1 mg/ml ampicillin, 0.1 mg/ml X-gal and 1 mmol/l isopropyl-β-D-thiogalactopyranoside (IPTG) and cultured at 37°C overnight.

[0344] The transformant obtained from colonies formed on the plate medium was stationarily cultured in a 96-well titer plate having 0.05 ml of LB medium containing 0.1 mg/ml ampicillin at 37°C overnight. Then, 0.05 ml of LB medium containing 20% glycerol was added thereto, followed by stirring to obtain a glycerol stock.

(3) Construction of cosmid library

[0345] About 0.1 mg of the genome DNA of *Corynebacterium glutamicum* ATCC 13032 was partially digested with *Sau*3AI (manufactured by Takara Shuzo) and then ultracentrifuged (26,000 rpm, 18 hours, 20°C) under 10 to 40% sucrose density gradient obtained using 10% and 40% sucrose buffers (1 mol/l NaCl, 20 mmol/l Tris hydrochloride, 5 mmol/l EDTA, 10% or 40% sucrose, pH 8.0). After the centrifugation, the solution thus separated was fractionated into tubes at 1 ml in each tube. After confirming the DNA fragment length of each fraction by agarose gel electrophoresis, a fraction containing a large amount of DNA fragment of about 40 kb was precipitated with ethanol.

[0346] The DNA fragment was ligated to the *Bam*HI site of superCos1 (manufactured by Stratagene) in accordance with the manufacture's instructions. The ligation product was incorporated into *Escherichia coli* XL-1-BlueMR strain (manufactured by Stratagene) using Gigapack III Gold Packaging Extract (manufactured by Stratagene) in accordance with the manufacture's instructions. The *Escherichia coli* was spread on LB plate medium containing 0.1 mg/ml ampicillin and cultured therein at 37°C overnight to isolate colonies. The resulting colonies were stationarily cultured at 37°C overnight in a 96-well titer plate containing 0.05 ml of the LB medium containing 0.1 mg/ml ampicillin in each well. LB medium containing 20% glycerol (0.05 ml) was added thereto, followed by stirring to obtain a glycerol stock.

(4) Determination of nucleotide sequence

(4-1) Preparation of template

[0347] The full nucleotide sequence of *Corynebacterium glutamicum* ATCC 13032 was determined mainly based on the whole genome shotgun method. The template used in the whole genome shotgun method was prepared by the PCR method using the library prepared in the above (2).

[0348] Specifically, the clone derived from the whole genome shotgun library was inoculated using a replicator (manufactured by GENETIX) into each well of a 96-well plate containing the LB medium containing 0.1 mg/ml of ampicillin at 0.08 ml per each well and then stationarily cultured at 37°C overnight.

[0349] Next, the culturing solution was transported using a copy plate (manufactured by Tokken) into a 96-well reaction plate (manufactured by PE Biosystems) containing a PCR reaction solution (TaKaRa Ex Taq (manufactured by Takara Shuzo)) at 0.08 ml per each well. Then, PCR was carried out in accordance with the protocol by Makino *et al.* (*DNA Research*, 5: 1-9 (1998)) using GeneAmp PCR System 9700 (manufactured by PE Biosystems) to amplify the inserted fragment.

[0350] The excessive primers and nucleotides were eliminated using a kit for purifying a PCR production (manufactured by Amersham Pharmacia Biotech) and the residue was used as the template in the sequencing reaction.

[0351] Some nucleotide sequences were determined using a double-stranded DNA plasmid as a template.

[0352] The double-stranded DNA plasmid as the template was obtained by the following method

[0353] The clone derived from the whole genome shotgun library was inoculated into a 24- or 96-well plate containing a 2 · YT medium (16 g/l bactotryptor. 10 g/l yeast extract. 5 g/ sodium chloride. pH 7.0) containing 0.05 mg/ml ampicillin at 1.5 ml per each well and then cultured under shaking at 37°C overnight.

[0354] The double-stranded DNA plasmid was prepared from the culturing solution using an automatic plasmid preparing machine. KURABO PI-50 (manufactured by Kurabo Industries) or a multiscreen (manufactured by Millipore) in accordance with the protocol provided by the manufacturer.

[0355] To purify the double-stranded DNA plasmid using the multiscreen. Biomek 2000 (manufactured by Beckman Coulter) or the like was employed.

[0356] The thus obtained double-stranded DNA plasmid was dissolved in water to give a concentration of about 0.1 mg/ml and used as the template in sequencing.

(4-2) Sequencing reaction

[0357] To 6 µl of a solution of ABI PRISM BigDye Terminator Cycle Sequencing Ready Reaction Kit (manufactured by PE Biosystems). an M13 regular direction primer (M13-21) or an M13 reverse direction primer (M13REV) (*DNA Research, 5*: 1-9 (1998) and the template prepared in the above (4-1) (the PCR product or the plasmid) were added to give 10 µl of a sequencing reaction solution. The primers and the templates were used in an amount of 1.6 pmol and an amount of 50 to 200 ng. respectively.

[0358] Dye terminator sequencing reaction of 45 cycles was carried out with GeneAmp PCR System 9700 (manufactured by PE Biosystems) using the reaction solution. The cycle parameter was determined in accordance with the manufacturer's instruction accompanying ABI PRISM BigDye Terminator Cycle Sequencing Ready Reaction Kit. The sample was purified using MultiScreen HV plate (manufactured by Millipore) according to the manufacture's instructions. The thus purified reaction product was precipitated with ethanol. followed by drying. and then stored in the dark at -30°C.

[0359] The dry reaction product was analyzed by ABI PRISM 377 DNA Sequencer and ABI PRISM 3700 DNA Analyzer (both manufactured by PE Biosystems) each in accordance with the manufacture's instructions.

[0360] The data of about 50.000 sequences in total (i.e.. about 42.000 sequences obtained using 377 DNA Sequencer and about 8.000 reactions obtained by 3700 DNA Analyser) were transferred to a server (Alpha Server 4100: manufactured by COMPAQ) and stored. The data of these about 50,000 sequences corresponded to 6 times as much as the genome size.

(5) Assembly

[0361] All operations were carried out on the basis of UNIX platform. The analytical data were output in Macintosh platform using X Window System. The base call was carried out using phred (The University of Washington). The vector sequence data was deleted using SPS Cross_Match (manufactured by Southwest Parallel Software). The assembly was carried out using SPS phrap (manufactured by Southwest Parallel Software: a high-speed version of phrap (The University of Washington)). The contig obtained by the assembly was analyzed using a graphical editor. consed (The University of Washington). A series of the operations from the base call to the assembly were carried out simultaneously using a script phredPhrap attached to consed.

(6) Determination of nucleotide sequence in gap part

[0362] Each cosmid in the cosmid library constructed in the above (3) was prepared by a method similar to the preparation of the double-stranded DNA plasmid described in the above (4-1). The nucleotide sequence at the end of the inserted fragment of the cosmid was determined by using ABI PRISM BigDye Terminator Cycle Sequencing Ready Reaction Kit (manufactured by PE Biosystems) according to the manufacture's instructions.

[0363] About 800 cosmid clones were sequenced at both ends to search a nucleotide sequence in the contig derived from the shotgun sequencing obtained in the above (5) coincident with the sequence. Thus. the linkage between respective cosmid clones and respective contigs were determined and mutual alignment was carried out. Furthermore. the results were compared with the physical map of *Corynebacterium glutamicum* ATCC 13032 (*Mol. Gen. Genet., 252*: 255-265 (1996) to carrying out mapping between the cosmids and the contigs.

[0364] The sequence in the region which was not covered with the contigs was determined by the following method.

[0365] Clones containing sequences positioned at the ends of contigs were selected. Among these clones. about 1.000 clones wherein only one end of the inserted fragment had been determined were selected and the sequence at the opposite end of the inserted fragment was determined. A shotgun library clone or a cosmid clone containing the sequences at the respective ends of the inserted fragment in two contigs was identified. the full nucleotide sequence

of the inserted fragment of this clone was determined, and thus the nucleotide sequence of the gap part was determined. When no shotgun library clone or cosmid clone covering the gap part was available, primers complementary to the end sequences at the two contigs were prepared and the DNA fragment in the gap part was amplified by PCR. Then, sequencing was performed by the primer walking method using the amplified DNA fragment as a template or by the shotgun method in which the sequence of a shotgun clone prepared from the amplified DNA fragment was determined. Thus, the nucleotide sequence of the domain was determined.

[0366] In a region showing a low sequence precision, primers were synthesized using AUTOFINISH function and NAVIGATING function of consed (The University of Washington) and the sequence was determined by the primer walking method to improve the sequence precision. The thus determined full nucleotide sequence of the genome of *Corynebacterium glutamicum* ATCC 13032 strain is shown in SEQ ID NO:1.

(7) Identification of ORF and presumption of its function

[0367] ORFs in the nucleotide sequence represented by SEQ ID NO:1 were identified according to the following method. First, the ORF regions were determined using software for identifying ORF, i.e., Glimmer, GeneMark and GeneMark.hmm on UNIX platform according to the respective manual attached to the software.

[0368] Based on the data thus obtained, ORFs in the nucleotide sequence represented by SEQ ID NO:1 were identified.

[0369] The putative function of an ORF was determined by searching the homology of the identified amino acid sequence of the ORF against an amino acid database consisting of protein-encoding domains derived from Swiss-Prot, PIR or Genpept database constituted by protein encoding domains derived from GenBank database. Frame Search (manufactured by Compugen), or by searching the homology of the identified amino acid sequence of the ORF against an amino acid database consisting of protein-encoding domains derived from Swiss-Prot, PIR or Genpept database constituted by protein encoding domains derived from GenBank database, BLAST. The nucleotide sequences of the thus determined ORFs are shown in SEQ ID NOS:2 to 3501, and the amino acid sequences encoded by these ORFs are shown in SEQ ID NOS:3502 to 7001.

[0370] In some cases of the sequence listings in the present invention, nucleotide sequences, such as TTG, TGT, GGT, and the like, other than ATG, are read as an initiating codon encoding Met.

[0371] Also, the preferred nucleotide sequences are SEQ ID NOS:2 to 355 and 357 to 3501, and the preferred amino acid sequences are shown in SEQ ID NOS:3502 to 3855 and 3857 to 7001

[0372] Table 1 shows the registration numbers in the above-described databases of sequences which were judged as having the highest homology with the nucleotide sequences of the ORFs as the results of the homology search in the amino acid sequences using the homology-searching software Frame Search (manufactured by Compugen), names of the genes of these sequences, the functions of the genes, and the matched length, identities and analogies compared with publicly known amino acid translation sequences. Moreover, the corresponding positions were confirmed via the alignment of the nucleotide sequence of an arbitrary ORF with the nucleotide sequence of SEQ ID NO: 1. Also, the positions of nucleotide sequences other than the ORFs (for example, ribosomal RNA genes, transfer RNA genes, IS sequences, and the like) on the genome were determined.

[0373] Fig. 1 shows the positions of typical genes of the *Corynebacterium glutamicum* ATCC 13032 on the genome.

Table 1

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
2	3502	1	1572	1572	gsp:R98523	Brevibacterium flavum dnaA	99.8	99.8	524	replication initiation protein DnaA
3	3503	1920	1597	324						
4	3504	2292	3473	1182	sp:DP3B_MYCSM	Mycobacterium smegmatis dnaN	50.5	81.8	390	DNA polymerase III beta chain
5	3505	3585	4766	1182	sp:RECF_MYCSM	Mycobacterium smegmatis recF	53.3	79.9	392	DNA replication protein (recF protein)
6	3506	4766	5299	534	sp:YREG_STRCO	Streptomyces coelicolor yreG	35.1	58.1	174	hypothetical protein
7	3507	5354	7486	2133	pir:S44198	Mycobacterium tuberculosis H37Rv gyrB	71.9	88.9	704	DNA topoisomerase (ATP hydrolyzing)
8	3508	7830	8795	966						
9	3509	9466	8798	669						
10	3510	9562	10071	510						
11	3511	9914	9474	441						
12	3512	11177	10107	1071	sp:YV11_MYCTU	Mycobacterium tuberculosis H37Rv	29.4	50.7	422	NAGC/XYLR repressor
13	3513	11523	11263	261						
14	3514	11768	11523	246						
15	3515	11831	14398	2568	sp:GYRA_MYCTU	Mycobacterium tuberculosis H37Rv Rv0006 gyrA	70.4	88.1	854	DNA gyrase subunit A
16	3516	14405	14746	342	pir:E70698	Mycobacterium tuberculosis H37Rv Rv0007	29.5	69.6	112	hypothetical membrane protein
17	3517	16243	15209	1035	sp:YEIH_ECOLI	Escherichia coli K12 yeiH	33.7	63.5	329	hypothetical protein
18	3518	16314	17207	894	gp:AB042619_1	Hydrogenophilus thermoluteolus TH-1 cbbR	27.6	62.3	268	bacterial regulatory protein, LysR type
19	3519	17251	17670	420						
20	3520	18729	17860	870	gp:AF156103_2	Rhodobacter capsulatus ccdA	29.1	57.4	265	cytochrome c biogenesis protein
21	3521	19497	18736	762	pir:A49232	Coxiella burnetii com1	31.6	64.5	155	hypothetical protein
22	3522	19705	20073	369	pir:E70664	Mycobacterium tuberculosis H37Rv Rv1846c	36.8	70.1	117	repressor

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Termina (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched ength (a.a.)	Function
23	3523	20073	21065	993	gp MLCB1788_6	Mycobacterium leprae MLCB1788.18	24.9	50.8	321	hypothetical membrane protein
24	3524	21253	21074	180	pir 40838	Corynebacterium sp. ATCC 31090	65.4	88.5	26	2,5-diketo-D-gluconic acic reductase
25	3525	21597	22124	528	sp 5NTD_VIBPA	Vibrio parahaemolyticus nutA	27.0	56.1	196	5'-nucleotidase precursor
26	3526	22164	23399	1236	gp AE001909_7	Deinococcus radiodurans DR0505	27.0	56.7	270	5'-nucleotidase family protein
27	3527	23779	23615	165	prf 2513302C	Corynebacterium striatum ORF1	52.9	72.6	51	transposase
28	3528	24295	24729	435	prf 2413353A	Xanthomonas campestris phaseoli ohr	51.8	79.9	139	organic hydroperoxide detoxication enzyme
29	3529	26297	24885	1413	sp RECG_THIFE	Thiobacillus ferrooxidans recG	32.7	60.8	217	ATP-dependent DNA helicase
30	3530	26338	26775	438						
31	3531	28099	26822	1278	sp AMYH_YEAST	Saccharomyces cerevisiae S288C YIR019C sta1	26.7	54.1	449	glucan 1,4-alpha-glucosidase
32	3532	29117	28164	954	gp ERU52850_1	Erysipelothrix rhusiopathiae ewlA	28.9	63.7	311	lipoprotein
33	3533	29965	29117	849	gp AF180520_3	Streptococcus pyogenes SF370 mtsC	34.6	74.1	266	ABC 3 transport family or integral membrane protein
34	3534	29995	30651	657	sp FECE_ECOLI	Escherichia coli K12 fecE	39.2	70.3	222	iron(III) dicitrate transport ATP-biding protein
35	3535	30697	31677	981	pir A72417	Thermotoga maritima MSB8 TM0114	25.8	56.5	283	sugar ABC transporter, periplasmic sugar-binding protein
36	3536	31677	32699	1023	prf 1207243B	Escherichia coli K12 rbsC	30.5	68.3	312	high affinity ribose transport protein
37	3537	32699	33457	759	sp RBSA_BACSU	Bacillus subtilis 168 rbsA	32.2	76.7	236	ribose transport ATP-binding protein
38	3538	34280	33465	816	pir I51116	Petromyzon marinus	23.6	44.4	347	neurofilament subunit NF-180
39	3539	34339	34899	561	sp CYPA_MYCTU	Mycobacterium leprae H37RV RV0009 ppiA	79.9	89.9	169	peptidyl-prolyl cis-trans isomerase A
40	3540	34982	35668	687	sp YQGP_BACSU	Bacillus subtilis 168 yqgP	29.2	53.1	226	hypothetical membrane protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
41	3541	37221	38198	978	sp FEPG_ECOLI	Escherichia coli K12 fepG	40.4	70.5	332	ferric enterobactin transport system permease protein
42	3542	37242	36247	996						
43	3543	38202	38978	777	gp VCU52150_9	Vibrio cholerae viuC	51.8	81.8	253	ATPase
44	3544	38978	39799	822	sp VIUB_VIBVU	Vibrio vulnificus MO6-24 viuB	26.2	52.7	260	vulnibactin utilization protein
45	3545	40458	40189	270	sp YO11_MYCTU	Mycobacterium tuberculosis H37Rv Rv0011c	40.0	72.6	95	hypothetical membrane protein
46	3546	42513	40576	1938	sp PKNB_MYCLE	Mycobacterium leprae pknB	40.6	68.7	648	serine/threonine protein kinase
47	3547	43919	42513	1407	gp AF094711_1	Streptomyces coelicolor pksC	31.7	59.1	486	serine/threonine protein kinase
48	3548	45347	43926	1422	gp AF241575_1	Streptomyces griseus pbpA	33.5	66.7	492	penicillin-binding protein
49	3549	46489	45347	1143	sp SP5E_BACSU	Bacillus subtilis 168 spoVE	31.2	65.6	375	stage V sporulation protein E
50	3550	48021	46669	1353	pir H70699	Mycobacterium tuberculosis H37Rv ppp	44.1	70.8	469	phosphoprotein phosphatase
51	3551	48485	48024	462	pir A70700	Mycobacterium tuberculosis H37Rv Rv0019c	38.7	66.5	155	hypothetical protein
52	3552	49368	48505	864	pir B70700	Mycobacterium tuberculosis H37Rv Rv0020c	23.6	38.8	526	hypothetical protein
53	3553	49601	49455	147						
54	3554	50616	49897	720						
55	3555	50972	50754	219						
56	3556	51436	50966	471						
57	3557	53055	54008	954	sp PH2M_TRICU	Trichosporon cutaneum ATCC 46490	29.9	63.3	117	phenol 2-monooxygenase
58	3558	53095	51626	1470	sp GABD_ECOLI	Escherichia coli K12 gabD	46.7	78.2	490	succinate-semialdehyde dehydrogenase (NAD(P)+)
59	3559	54080	55546	1467	sp YRKH_BACSU	Bacillus subtilis yrkH	27.3	57.0	242	hypothetical protein
60	3560	56417	55629	789	sp Y441_METJA	Methanococcus jannaschii MJ0441	29.0	64.1	262	hypothetical membrane protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nti	ORf (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
61	3561	56676	56386	291	sp YRKF_BACSU	Bacillus subtilis yrkF	40 5	74 3	74	hypothetical protein
62	3562	57270	56730	541	sp YC61_SYNY3	Synechocystis sp PCC6803 slr1261	36 3	70 4	179	hypothetical protein
63	3563	57478	57251	174	pir G70988	Mycobacterium tuberculosis H37Rv Rv1766	53 2	83 9	62	hypothetical protein
64	3564	58087	58941	855						
65	3565	59091	59930	840	gp LMFL4768_11	Leishmania major L4768 11	26 8	50 7	310	hypothetical protein
66	3566	59952	60662	711						
67	3567	60669	62321	1653						
68	3568	63508	62390	1119	pir F70952	Mycobacterium tuberculosis H37Rv Rv1239c corA	29 5	59 5	390	magnesium and cobalt transport protein
69	3569	64040	63594	447						
70	3570	64190	65458	1269	gp AF179611_12	Zymomonas mobilis ZM4 clcb	30.0	64.8	400	chloride channel protein
71	3571	66197	65508	690	sp PNUC_SALTY	Salmonella typhimurium pnuC	24 1	53 1	241	required for NMN transport
72	3572	66851	67972	1122	sp PHOL_MYCTU	Mycobacterium tuberculosis H37Rv RV2368C	29 1	60 0	340	phosphate starvation-induced protein-like protein
73	3573	68170	68301	132						
74	3574	68634	68251	384						
75	3575	69060	69824	765						
76	3576	70186	68720	1467	sp CITM_BACSU	Bacillus subtilis citM	42 3	68 8	497	Mg(2+)/citrate complex secondary transporter
77	3577	70500	72158	1653	sp DPIB_ECOLI	Escherichia coli K12 dpiB	27 2	60 6	563	two-component system sensor histidine kinase
78	3578	72043	71474	570						
79	3579	72161	72814	654	sp DPIA_ECOLI	Escherichia coli K12 criR	33 2	63 3	229	transcriptional regulator
80	3580	73728	72817	912	gp AF134895_1	Corynebacterium glutamicum unkdh	43 3	73 7	293	*D* isomer specific 2-hydroxyacid dehydrogenase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
81	3581	73844	74272	429	gp SCM2_3	Streptomyces coelicolor A3(2) SCM2.03	38.6	76.4	127	hypothetical protein
82	3582	74490	75491	1002	sp BIOB_CORGL	Corynebacterium glutamicum bioB	99.4	99.7	334	biotin synthase
83	3583	75506	75742	237	pir H70542	Mycobacterium tuberculosis H37Rv Rv1590	72.1	79.1	43	hypothetical protein
84	3584	75697	76035	339	sp YKI4_YEAST	Saccharomyces cerevisiae YKL084w	34.1	63.5	85	hypothetical protein
85	3585	76353	76469	117						
86	3586	80753	80613	141	PIR F81737	Chlamydia muridarum Nigg TC0129	71.0	75.0	42	hypothetical protein
87	3587	81274	81002	273	GSP:Y35814	Chlamydia pneumoniae	61.0	66.0	84	hypothetical protein
88	3588	83668	82120	1449	prf 2512333A	Streptomyces virginiae varS	25.6	59.0	507	integral membrane efflux protein
89	3589	84936	83691	1245	gp D38505_1	Bacillus sp	97.2	99.8	394	creatinine deaminase
90	3590	85403	85098	306						
91	3591	86277	85663	615						
92	3592	86318	87241	924	sp HST2_YEAST	Saccharomyces cerevisiae hst2	26.2	50.2	279	SIR2 gene family (silent information regulator)
93	3593	88532	87561	972	prf 2316378A	Propionibacterium acnes	30.7	59.0	251	triacylglycerol lipase
94	3594	89444	88545	900	prf 2316378A	Propionibacterium acnes	29.4	56.1	262	triacylglycerol lipase
95	3595	89558	90445	888						
96	3596	90973	90461	513	gp AB029154_1	Corynebacterium glutamicum ureR	90.6	94.7	171	transcriptional regulator
97	3597	91174	91473	300	gp AB029154_2	Corynebacterium glutamicum ureA	100.0	100.0	100	urease gammma subunit or urease structural protein
98	3598	91503	91988	486	gp CGL251883_2	Corynebacterium glutamicum ATCC 13032 ureB	100.0	100.0	162	urease beta subunit
99	3599	91992	93701	1710	gp CGL251883_3	Corynebacterium glutamicum ATCC 13032 ureC	100.0	100.0	570	urease alpha subunit

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
100	3600	93729	94199	471	gp:CGL251883_4	Corynebacterium glutamicum ATCC 13032 ureE	100.0	100.0	157	urease accessory protein
101	3601	94207	94879	678	gp:CGL251883_5	Corynebacterium glutamicum ATCC 13032 ureF	100.0	100.0	226	urease accessory protein
102	3602	94899	95513	615	gp:CGL251883_6	Corynebacterium glutamicum ATCC 13032 ureG	100.0	100.0	205	urease accessory protein
103	3603	95517	96365	849	gp:CGL251883_7	Corynebacterium glutamicum ATCC 13032 ureD	100.0	100.0	283	urease accessory protein
104	3604	97144	96368	777	prf:2318326B	Agrobacterium radiobacter echA	21.2	48.4	279	epoxide hydrolase
105	3605	97521	98189	669						
106	3606	98470	97319	1152	gp:AF148322_1	Streptomyces viridifaciens vlmF	26.5	59.7	347	valanimycin resistant protein
107	3607	99819	100493	675						
108	3608	101582	98808	2775						
109	3609	103435	101612	1824	sp:HTPG_ECOLI	Escherichia coli K12 htpG	23.8	52.7	668	heat shock protein (hsp90-family)
110	3610	103494	104909	1416	sp:AMN_ECOLI	Escherichia coli K12 amn	41.0	68.2	481	AMP nucleosidase
111	3611	105751	105173	579						
112	3612	106392	105841	552	pir:E72483	Aeropyrum pernix K1 APE2509	29.6	58.7	196	acetolactate synthase large subunit
113	3613	107289	106630	660						
114	3614	107435	110890	3456	sp:PUTA_SALTY	Salmonella typhimurium putA	25.8	50.4	1297	proline dehydrogenase/P5C dehydrogenase
115	3615	111161	111274	114						
116	3616	111374	112318	945	sp:AAD_PHACH	Phanerochaete chrysosporium aad	30.2	60.7	338	aryl-alcohol dehydrogenase (NADP+)
117	3617	112470	114083	1614	sp:YDAH_ECOLI	Escherichia coli K12 ydaH	36.5	71.4	513	pump protein (transport)
118	3618	114147	115478	1332	prf:2422424A	Enterobacter agglomerans	23.0	49.2	352	indole-3-acetyl-Asp hydrolase
119	3619	115262	114564	699						
120	3620	115578	115943	366	sp:YIDH_ECOLI	Escherichia coli K12 yidH	35.9	70.8	106	hypothetical membrane protein
121	3621	115949	116263	315						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
122	3622	118599	116548	2052						
123	3623	119589	118810	780	sp ACCR_AGRTU	Agrobacterium tumefaciens accR	29.5	59.7	258	transcriptional repressor
124	3624	120021	120410	390	pir C70019	Bacillus subtilis yurT	57.9	78.6	126	methylglyoxalase
125	3625	120922	120413	510	sp YC76_MYCTU	Mycobacterium tuberculosis H37Rv Rv1276c	37.0	64.8	162	hypothetical protein
126	3626	122459	120951	1509	prf 2309180A	Pseudomonas fluorescens mtlD	43.5	70.4	497	mannitol dehydrogenase
127	3627	123841	122507	1335	prf 2321326A	Klebsiella pneumoniae dalT	30.3	68.3	435	D-arabinitol transporter
128	3628	123842	124030	189						
129	3629	124130	124966	837	sp GATR_ECOLI	Escherichia coli K12 gatR	27.3	64.6	260	galactitol utilization operon repressor
130	3630	124932	126350	1419	sp XYLB_STRRU	Streptomyces rubiginosus xylB	45.0	68.1	451	xylulose kinase
131	3631	127171	127992	822						
132	3632	127189	126353	837	gp CGPAN_2	Corynebacterium glutamicum ATCC 13032 panC	100.0	100.0	279	pantoate--beta-alanine ligase
133	3633	128004	127192	813	gp CGPAN_1	Corynebacterium glutamicum ATCC 13032 panB	100.0	100.0	271	3-methyl-2-oxobutanoate hydroxymethyltransferase
134	3634	129049	128099	951						
135	3635	130118	129489	630	sp 3MG_ARATH	Arabidopsis thaliana mag	42.0	67.6	186	DNA-3-methyladenine glycosylase
136	3636	130145	130798	654						
137	3637	131738	130815	924	gp AB029896_1	Petroleum degrading bacterium HD-1 hde	39.3	69.3	270	esterase
138	3638	131798	132424	627						
139	3639	132424	132981	558	sp CAH_METTE	Methanosarcina thermophila	30.9	53.2	201	carbonate dehydratase
140	3640	134113	132971	1143	sp XYLR_BACSU	Bacillus subtilis W23 xylR	24.1	49.3	357	xylose operon repressor protein
141	3641	135478	134207	1272	gp LLLP4214_12	Lactococcus lactis mef214	21.1	61.2	418	macrolide efflux protein
142	3642	136321	135518	804						
143	3643	136565	136122	444						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
144	3644	136804	138744	1941						
145	3645	138791	140329	1539						
146	3646	139861	139226	636						
147	3647	140329	141789	1461	pir I39714	Agrobacterium tumefaciens celA	24.3	51.2	420	cellulose synthase
148	3648	141796	143526	1731	sp HKR1_YEAST	Saccharomyces cerevisiae YDR420W hkr1	25.1	51.8	593	hypothetical membrane protein
149	3649	142455	143075	621						
150	3650	143575	144639	1065						
151	3651	144725	145480	756						
152	3652	146396	145518	879	sp RARD_PSEAE	Pseudomonas aeruginosa rarD	34.7	60.7	303	chloramphenicol sensitive protein
153	3653	146522	147238	717	sp YADS_ECOLI	Escherichia coli K12 yadS	30.3	59.1	198	hypothetical membrane protein
154	3654	147238	147570	333						
155	3655	148122	149780	1659						
156	3656	150930	149794	1137	sp ABRB_ECOLI	Escherichia coli K12 abrB	32.4	62.3	361	transport protein
157	3657	151572	152369	798	sp YFCA_ECOLI	Escherichia coli K12 yfcA	34.7	70.2	248	hypothetical membrane protein
158	3658	151589	150966	624						
159	3659	152410	152814	405						
160	3660	155613	153226	2388	sp HRPB_ECOLI	Escherichia coli K12 hrpB	33.8	64.3	829	ATP-dependent helicase
161	3661	155853	156167	315						
162	3662	156821	156147	675	sp NODL_RHILV	Rhizobium leguminosarum bv. viciae plasmid pRL1JI nodL	40.4	66.0	188	nodulation protein
163	3663	156848	157537	690	sp ALKB_ECOLI	Escherichia coli o373#1 alkB	34.7	60.7	219	DNA repair system specific for alkylated DNA
164	3664	157614	158138	525	sp 3MG1_ECOLI	Escherichia coli K12 tag	39.8	65.1	166	DNA-3-methyladenine glycosylase
165	3665	158154	158831	678	sp RHTC_ECOLI	Escherichia coli K12 rhtC	34.1	61.3	217	*threonine* efflux protein
166	3666	158869	159159	291	sp YAAA_BACSU	Bacillus subtilis yaaA	50.9	72.7	55	hypothetical protein
167	3667	159162	160013	852	prf 2510326B	Streptomyces peucetius dnrV	31.0	52.1	284	doxorubicin biosynthesis enzyme

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
168	3668	160029	160370	342	gp SPAC1250_3	Schizosaccharomyces pombe SPAC1250.04c	35.6	56.7	104	methyltransferase
169	3669	160431	161360	930						
170	3670	161696	162352	657						
171	3671	162295	161363	933						
172	3672	162463	162867	405	gp AE002420_13	Neisseria meningitidis MC58 NMB0662	41.5	76.3	118	ribonuclease
173	3673	162965	163603	639						
174	3674	165717	166457	741						
175	3675	165755	163689	2067	gp AF176569_1	Mus musculus nl1	28.5	57.2	722	neprilysin-like metallopeptidase 1
176	3676	166457	167419	963						
177	3677	168595	167837	759	sp FARR_ECOLI	Escherichia coli K12 farR	29.8	65.6	238	transcriptional regulator, GntR family or fatty acyl-responsive regulator
178	3678	168975	169991	1017	pir T14544	Beta vulgaris	28.6	63.0	332	fructokinase or carbohydrate kinase
179	3679	169996	170916	921	gp SC8F11_3	Streptomyces coelicolor A3(2) SC8F11.03c	52.7	80.7	296	hypothetical protein
180	3680	170933	172444	1512	prf 2204281A	Streptomyces coelicolor msdA	61.0	86.1	498	methylmalonic acid semialdehyde dehydrogenase
181	3681	172468	173355	888	sp IOLB_BACSU	Bacillus subtilis iolB	33.2	58.2	268	myo-inositol catabolism
182	3682	173548	175275	1728	sp IOLD_BACSU	Bacillus subtilis iolD	41.0	69.8	586	myo-inositol catabolism
183	3683	175319	176272	954	sp MOCC_RHIME	Rhizobium meliloti mocC	29.7	51.0	290	rhizopine catabolism protein
184	3684	176308	177318	1011	sp MI2D_BACSU	Bacillus subtilis idh or iolG	39.1	72.2	335	myo inositol 2 dehydrogenase
185	3685	177334	178203	870	sp IOLH_BACSU	Bacillus subtris iolH	44.6	72.1	287	myo-inositol catabolism
186	3686	178285	179658	1374	sp TCMA_STRGA	Streptomyces glaucescens tcmA	30.9	61.5	457	metabolite export pump of tetracenomycin C resistance
187	3687	179081	178461	621						
188	3688	179689	180711	1023	sp YVAA_BACSU	Bacillus subtilis yvaA	31.1	65.5	354	oxidoreductase
189	3689	180842	181297	456						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
190	3690	181264	181647	384						
191	3691	182670	181687	393	gp SRF9798_1	Streptomyces reticuli cebR	32.0	61.9	331	regulatory protein
192	3692	182819	184051	1233	sp Y4HM_RHISN	Rhizobium sp. NGR234 y4hM	24.4	52.5	442	oxidoreductase
193	3693	184077	185087	1011	sp YFIH_BACSU	Bacillus subtilis yfiH	33.7	64.7	303	hypothetical protein
194	3694	185214	185642	429						
195	3695	186508	186708	201	sp CSP_ARTGO	Streptomyces coelicolor A3(2) csp	70.3	92.2	64	cold shock protein
196	3696	186769	187302	534						
197	3697	187302	187607	306						
198	3698	187687	188100	414	prf 2113413A	Stellaria longipes	30.6	58.2	134	caffeoyl-CoA 3-O-methyltransferase
199	3699	188725	188300	426						
200	3700	189736	188747	990	sp CCPA_BACSU	Bacillus subtilis ccpA	28.7	62.1	338	glucose-resistance amylase regulator regulator
201	3701	189920	190321	402						
202	3702	190628	190389	240						
203	3703	192175	190703	1473	sp XYLT_LACBR	Lactobacillus brevis xylT	36.0	70.5	458	D-xylose proton symporter
204	3704	193248	192949	300						
205	3705	193362	194464	1203	gp AF189147_1	Corynebacterium glutamicum ATCC 13032 tnp	100.0	100.0	401	transposase (ISCg2)
206	3706	195038	194604	435	sp FIXL_RHIME	Rhizobium meliloti fxL	27.6	60.7	145	signal-transducing histidine kinase
207	3707	195240	199769	4530	gp AB024708_1	Corynebacterium glutamicum gltB	99.9	100.0	1510	glutamine 2-oxoglutarate aminotransferase large subunit
208	3708	199772	201289	1518	gp AB024708_2	Corynebacterium glutamicum gltD	99.4	99.8	506	glutamine 2-oxoglutarate aminotransferase small subunit
209	3709	201580	201341	240						
210	3710	203244	201760	1485	pir C70793	Mycobacterium tuberculosis H37Rv Rv3698	44.6	72.8	496	hypothetical protein
211	3711	205588	205956	369						

Table 1 (continued)

SEQ NO. (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
212	3712	206068	206385	318						
213	3713	207011	203541	3471	prf 2224383C	Mycobacterium avium embB	39.8	70.6	1122	arabinosyl transferase
214	3714	208989	207007	1983	pir D70697	Mycobacterium tuberculosis H37Rv Rv3792	35.0	66.1	651	hypothetical membrane protein
215	3715	209968	209210	759	prf 2504279B	Pseudomonas sp phbB	31.4	56.5	223	acetoacetyl CoA reductase
216	3716	211455	209992	1464	pir B70697	Mycobacterium tuberculosis H37Rv Rv3790	66.0	85.1	464	oxidoreductase
217	3717	211768	211535	234						
218	3718	211777	212283	507						
219	3719	212283	212735	453						
220	3720	212656	213657	1002	gp LMA243459_1	Leishmania major ppg1	24.3	57.4	350	proteophosphoglycan
221	3721	213712	214107	396	sp Y0GN_MYCTU	Mycobacterium tuberculosis H37Rv Rv3789	60.5	83.9	124	hypothetical protein
222	3722	214121	214522	402						
223	3723	214527	215159	633	pir H70666	Mycobacterium tuberculosis H37Rv Rv1864c	43.2	73.8	206	hypothetical protein
224	3724	216100	215162	939	pir B70696	Mycobacterium tuberculosis H37Rv Rv3782 rfbE	63.6	79.1	302	rhamnosyl transferase
225	3725	216264	216605	342						
226	3726	216712	216116	597	gp AB016260_100	Agrobacterium tumefaciens plasmid pTi-SAKURA tiorf100	31.3	55.1	214	hypothetical protein
227	3727	217929	217141	789	sp RFBE_YEREN	Yersinia enterocolitica rfbE	47.0	78.4	236	O-antigen export system ATP-binding protein
228	3728	218746	217943	804	sp RFBD_YEREN	Yersinia enterocolitica rfbD	31.3	75.6	262	O-antigen export system permease protein
229	3729	218979	220151	1173	pir F70695	Mycobacterium tuberculosis H37Rv Rv3778c	36.5	63.0	416	hypothetical protein
230	3730	221107	220154	954	gp AF010309_1	Homo sapiens pig3	41.1	71.5	302	NADPH quinone oxidoreductase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
231	3731	221712	221131	582						
232	3732	221911	222207	297	PIR A70606	Mycobacterium tuberculosis H37Rv Rv3571	35.0	51.0	78	probable electron transfer protein
233	3733	223685	222210	1476	sp.ALST_BACSU	Bacillus subtilis alsT	46.7	75.8	475	amino acid carrier protein
234	3734	224336	225244	909						
235	3735	226324	225242	1083	gp.SYPCCMOEB_1	Synechococcus sp. PCC 7942 moeB	43.8	70.1	368	molybdopterin biosynthesis protein moeB (sulfurylase)
236	3736	226767	226312	456	prf.2403296D	Arthrobacter nicotinovorans moaE	44.7	75.3	150	molybdopterin synthase, large subunit
237	3737	227230	226760	471	sp.MOCB_SYNP7	Synechococcus sp. PCC 7942 moaCB	33.5	63.3	158	molybdenum cofactor biosynthesis protein CB
238	3738	227685	227218	468	prf.2403296C	Arthrobacter nicotinovorans moaC	61.7	84.4	154	co-factor synthesis protein
239	3739	228887	227703	1185	gp.ANY10817_2	Arthrobacter nicotinovorans moeA	34.5	58.6	377	molybdopterin co-factor synthesis protein
240	3740	229613	229891	723	prf.2403296F	Arthrobacter nicotinovorans modB	44.1	70.5	227	hypothetical membrane protein
241	3741	230514	229711	804	prf.2403296E	Arthrobacter nicotinovorans modA	34.0	68.0	256	molybdate-binding periplasmic protein
242	3742	230608	230928	321	pir.D70816	Mycobacterium tuberculosis H37Rv moaD2	37.5	70.8	96	molybdopterin converting factor subunit 1
243	3743	231842	230931	912	prf.2518354A	Thermococcus litoralis malK	34.3	60.8	365	maltose transport protein
244	3744	232267	231848	420	sp.YPT3_STRCO	Streptomyces coelicolor A3(2) ORF3	36.4	76.9	121	hypothetical membrane protein
245	3745	233282	232260	1023	sp.HIS8_ZYMMO	Zymomonas mobilis hisC	37.3	65.8	330	histidinol-phosphate aminotransferase
246	3746	233913	234818	906						
247	3747	235203	234910	294						
248	3748	235290	235409	120						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
249	3749	236212	235451	762	gp BAB8 286_1	Brucella abortus oxyR	29 4	57 1	252	transcript on factor
250	3750	236326	237342	1017	sp ADH2_BACST	Bacillus stearothermophilus DSM 2334 adh	34 0	66 0	335	alcohol dehydrogenase
251	3751	237345	238145	801	sp PUO_MICRU	Micrococcus rubens puo	21 5	38 1	451	putrescine oxidase
252	3752	238176	239525	1350	prf 2305239A	Borrelia burgdorferi mgtE	30 9	68 5	444	magnesium ion transporter
253	3753	239772	239945	174						
254	3754	239986	241515	1530	prf 2320140A	Xenopus laevis	33 2	59 6	567	Na/dicarboxylate cotransporter
255	3755	242932	241883	1020	pir C70800	Mycobacterium tuberculosis H37Rv ty'A	46 1	69 1	317	oxidoreductase
256	3756	242910	243431	522	pir B70800	Mycobacterium tuberculosis H37Rv Rv3753c	48 8	73 8	160	hypothetical protein
257	3757	243494	243910	417	gp RHBNFXP_1	Bradyrhizobium japonicum	45 1	70 1	144	nitrogen fixation protein
258	3758	244015	244215	201						
259	3759	244466	244816	351						
260	3760	244902	247304	2403	sp YV34_MYCTU	Mycobacterium tuberculosis H37Rv Rv0507 mmpL2	20 7	45 7	997	membrane transport protein
261	3761	247310	248572	1263	sp TGT_ZYMMO	Zymomonas mobilis	41 3	68 0	400	queuine tRNA-ribosyltransferase
262	3762	249294	248557	738	sp YPDP_BACSU	Bacillus subtilis ypdP	28 1	62 1	203	hypothetical membrane protein
263	3763	249428	250507	1080						
264	3764	250369	249722	648						
265	3765	250503	251939	1437	p r S65588	Streptomyces glaucescens strW	24 3	49 6	526	ABC transporter
266	3766	251952	252830	879	sp SYE_BACSU	Bacillus subtilis gltX	34 8	63 3	316	glutamyl tRNA synthetase
267	3767	253819	252830	990						
268	3768	255438	254329	1110	gp PSESTBCBAD_1	Pseudomonas syringae tnpA	34 2	55 0	360	transposase
269	3769	255794	255492	303						
270	3770	256067	256204	138						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (aa)	nitial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (aa)	Function
271	3771	256599	257894	1296	gsp W69554	Brevibacterium lactofermentum aspC	98.6	100.0	432	aspartate transaminase
272	3772	257900	258529	630						
273	3773	258551	260875	2325	gp AF025391_1	Thermus thermophilus dnaX	31.6	53.1	642	DNA polymerase III holoenzyme tau subunit
274	3774	259312	258596	717						
275	3775	260987	261295	309	sp YAAK_BACSU	Bacillus subtilis yaaK	41.6	74.3	101	hypothetical protein
276	3776	261402	262055	654	sp RECR_BACSU	Bacillus subtilis recR	42.5	72.4	214	recombination protein
277	3777	263295	262546	750	prf 2503462B	Heliobacillus mobilis cobQ	38.3	61.7	248	cobyric acid synthase
278	3778	264500	263208	1269	prf 2503462C	Heliobacillus mobilis murC	31.3	60.6	444	UDP-N-acetylmuramyl tripeptide synthetase
279	3779	265678	264599	1080	pir H70794	Mycobacterium tuberculosis H37Rv dnaQ	25.7	55.2	346	DNA polymerase III epsilon chain
280	3780	269124	268258	867	sp YLEU_CORGL	Corynebacterium glutamicum (Brevibacterium flavum) ATCC 13032 orfX	100.0	100.0	270	hypothetical membrane protein
281	3781	269371	270633	1263	sp AKAB_CORGL	Corynebacterium glutamicum lysC-alpha	99.5	99.8	421	aspartate kinase alpha chain
282	3782	270576	269524	1053						
283	3783	271761	273194	1434						
284	3784	274128	273542	579	prf 2312309A	Mycobacterium smegmatis sigE	31.2	63.5	189	extracytoplasmic function alternative sigma factor
285	3785	274366	275871	1506	sp CATV_BACSU	Bacillus subtilis katA	52.9	76.4	492	vegetative catalase
286	3786	275891	276232	342						
287	3787	276247	275957	291						
288	3788	276703	276302	402	sp LRP_KLEPN	Klebsiella pneumoniae lrp	37.1	72.0	143	leucine-responsive regulatory protein
289	3789	276829	277581	753	sp AZLC_BACSU	Bacillus subtilis 1A1 azlC	30.5	68.0	203	branched chain amino acid transport

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
290	3790	277581	277904	324						
291	3791	278301	277987	315						
292	3792	279732	278388	345	gp AF178758_1	Sinorhizobium sp. As4 arsR	34.4	68.9	90	metalloregulatory protein
293	3793	278814	279893	1080	gp AF178758_2	Sinorhizobium sp. As4 arsB	52.2	84.2	341	arsenic oxyanion-translocation pump membrane subunit
294	3794	279393	280279	887	sp ARSC_STAXY	Staphylococcus xylosus arsC	31.1	68.9	119	arsenate reductase
295	3795	280666	280349	318						
296	3796	280939	280670	270						
297	3797	281401	280949	453						
298	3798	282933	281404	1530	gp AF097740_4	Bacillus firmus OF4 mrpD	32.4	70.4	503	Na+/H+ antiporter or multiple resistance and pH regulation related protein D
299	3799	283317	282937	381	prf 2504285D	Staphylococcus aureus mnhC	37.0	70.6	119	Na+/H+ antiporter
300	3800	285202	283317	2886	gp AF097740_1	Bacillus firmus OF4 mrpA	34.1	64.3	824	Na+/H+ antiporter or multiple resistance and pH regulation related protein A
301	3801	286373	287857	1485						
302	3802	287661	287059	603						
303	3803	288829	287966	864						
304	3804	289796	289131	666	sp CZCR_ALCEU	Alcaligenes eutrophus CH34 czcR	38.6	70.4	223	transcriptional activator
305	3805	291243	289777	1467	prf 2214304B	Mycobacterium tuberculosis mtrB	26.7	56.8	521	two-component system sensor histidine kinase
306	3806	291815	292417	603	sp APL_LACLA	Lactococcus lactis MG1363 apl	28.3	60.0	180	alkaline phosphatase
307	3807	291833	291273	561						
308	3808	293511	292597	915	pir B69865	Bacillus subtilis ykuE	26.1	54.7	307	phosphoesterase
309	3809	293539	293991	453	sp YQEY_BACSU	Bacillus subtilis yqeY	37.6	71.8	149	hypothetical protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
310	3810	296388	294004	2385	prf 2209359A	Mycobacterium leprae pon1	48.3	77.1	782	class A penicillin-binding protein(PBP1)
311	3811	297064	297402	339	pir S20912	Streptomyces coelicolor A3(2) whiB	40.9	63.4	71	regulatory protein
312	3812	297431	297622	192						
313	3813	297631	297783	153	gp SCH17_10	Streptomyces coelicolor A3(2) SCH17.10c	84.0	96.0	50	hypothetical protein
314	3814	297792	298250	459	pir G70790	Mycobacterium tuberculosis H37Rv Rv3678c	65.1	89.9	149	transcriptional regulator
315	3815	299084	298332	1353	sp SHIA_ECOLI	Escherichia coli K12 shiA	37.3	68.9	440	shikimate transport protein
316	3816	300087	300695	609						
317	3817	301261	299726	1536	sp LCFA_BACSU	Bacillus subtilis lcfA	31.1	59.9	534	long-chain-fatty-acid--CoA ligase
318	3818	302036	301512	525	gp SCJ4_28	Streptomyces coelicolor A3(2) SCJ4.28c	33.9	65.4	127	transcriptional regulator
319	3819	302167	303099	933	sp FABG_BACSU	Bacillus subtilis fabG	41.0	72.5	251	3-oxoacyl-(acyl-carrier-protein) reductase
320	3820	303133	304074	942	sp FLUG_EMENI	Emericella nidulans fluG	27.2	52.0	254	glutamine synthetase
321	3821	304070	305263	1194	prf 2512386A	Arabidopsis thaliana atg6	38.8	66.5	394	short-chain acyl CoA oxidase
322	3822	305288	305758	471	sp NODN_RHILV	Rhizobium leguminosarum nodN	45.8	72.6	153	nodulation protein
323	3823	305858	306700	843	pir F70790	Mycobacterium tuberculosis H37Rv Rv3677c	41.2	72.4	272	hydrolase
324	3824	306367	305195	1173						
325	3825	306800	307504	705						
326	3826	307402	306782	681	prf 2323349A	Vibrio cholerae crp	30.9	65.7	207	cAMP receptor protein
327	3827	307918	307727	192						
328	3828	307955	308734	780	sp UVEN_MICLU	Micrococcus luteus pdg	57.5	77.1	240	ultraviolet N-glycosylase/AP lyase
329	3829	308745	309302	558	pir B70790	Mycobacterium tuberculosis H37Rv Rv3673c	34.6	58.3	211	cytochrome c biogenesis protein

Table 1 (continued)

SEQ NO. (DNA)	SEQ NO (a a)	Initial (nt)	Termina (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a.)	Function
330	3830	309370	310038	669	sp YEAB_ECOLI	Escherichia coli K12 yeaB	30.7	56 3	192	hypothetical protein
331	3831	310135	311325	1191	pir H70789	Mycobacterium tuberculosis H37Rv Rv3671c	38.6	71 0	396	serine proteinase
332	3832	312891	311899	993	prf 2411250A	Corynebacterium sp. C12 cEH	29 6	52.1	280	epoxide hydrolase
333	3833	313457	312909	549	pir F70789	Mycobacterium tuberculosis H37Rv Rv3669	46 8	77.6	156	hypothetical membrane protein
334	3834	314590	313625	966	pir S72914	Mycobacterium leprae MTCY20G9.32C serB	29 6	65 5	287	phosphoserine phosphatase
335	3835	314980	316002	1023	pir E70788	Mycobacterium tuberculosis H37Rv Rv3660c	35 0	60 2	349	hypothetical protein
336	3836	316110	317132	1023	pir C44020	Escherich a coli trbB	32 9	66 5	319	conjugal transfer region protein
337	3837	316964	316350	615						
338	3838	317078	317893	816	pir C70788	Mycobacterium tuberculosis H37Rv Rv3658c	30 5	63 7	262	hypothetical membrane protein
339	3839	317920	318465	546	pir B70788	Mycobacterium tuberculosis H37Rv Rv3657c	33 8	64 2	201	hypothetical protein
340	3840	318492	318689	198	pir A70788	Mycobacterium tuberculosis H37Rv Rv3656c	47.5	84 8	59	hypothetical protein
341	3841	318696	319013	318						
342	3842	318958	318545	414						
343	3843	318991	319335	345						
344	3844	321690	319336	2355	sp YPRA_BACSU	Bacillus subtilis yprA	33 8	66 1	764	ATP-dependent RNA helicase
345	3845	322007	322207	201	sp CSP_ARTGO	Arthrobacter g obiformis SI55 csp	68.7	88 1	67	cold shock protein
346	3846	322216	321992	225						
347	3847	322910	325897	2988	pir G70563	Mycobacterium tuberculosis H37Rv Rv3646c topA	61.7	81 6	977	DNA topoisomerase I
348	3848	325904	326614	711						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
349	3849	327735	326695	1041	sp CYAB_STIAU	Stigmatella aurantiaca B17R20 cyaB	32.7	62.4	263	adenylate cyclase
350	3850	328283	329539	1257	sp DP3X_BACSU	Bacillus subtilis dnaX	25.3	52.7	423	DNA polymerase III subunit tau/gamma
351	3851	329748	329909	162						
352	3852	329933	330376	444	gp AE002103_3	Ureaplasma urealyticum uu033	32.6	59.0	144	hypothetical protein
353	3853	330873	331533	661	gp AE001882_8	Deinococcus radiodurans DR0202	39.0	63.4	172	hypothetical protein
354	3854	331552	332433	882	sp RLUC_ECOLI	Escherichia coli K12 rluC	43.6	65.0	314	ribosomal large subunit pseudouridine synthase C
355	3855	332919	334562	1644	sp BGLX_ERWCH	Erwinia chrysanthemi D1 bgxA	34.8	60.2	558	beta-glucosidase/xylosidase
356	3856	332965	334953	1989	gp AF090429_2	Azospirillum irakense salB	38.6	61.4	101	beta-glucosidase
357	3857	335009	336112	1104	sp FADH_AMYME	Amycolatopsis methanolica	66.6	86.5	362	NAD/mycothiol-dependent formaldehyde dehydrogenase
358	3858	335805	335185	621						
359	3859	336212	336748	537	sp YTH5_RHOSN	Rhodococcus erythropolis orf5	32.5	47.5	160	metallo-beta-lactamase superfamily
360	3860	336781	337449	669	sp FABG_ECOLI	Escherichia coli K12 fabG	25.9	55.8	251	3-oxoacyl-(acyl-carrier-protein) reductase
361	3861	337539	338768	1230	gp AF148322_1	Streptomyces viridifaciens vlmF	26.3	56.4	415	valanimycin resistant protein
362	3862	338793	339725	933	prf 2512357B	Actinoplanes sp. acbB	33.8	66.3	320	dTDP-glucose 4,6-dehydratase
363	3863	340569	340195	375	pir A70562	Mycobacterium tuberculosis H37Rv Rv3632	59.3	88.9	108	hypothetical protein
364	3864	341327	340569	759	sp YC22_METJA	Methanococcus jannaschii JAL-1 MJ1222	33.9	66.5	230	dolichol phosphate mannose synthase
365	3865	341347	342375	1029						
366	3866	342417	343451	1035	sp YEFJ_ECOLI	Escherichia coli K12 yefJ	25.8	57.3	260	nucleotide sugar synthetase
367	3867	343636	345717	2082	sp USHA_SALTY	Salmonella typhimurium ushA	26.1	54.4	586	UDP-sugar hydrolase
368	3868	345975	345814	162						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
369	3869	346460	346110	351						
370	3870	348019	346961	1059	sp ADH_MYCTU	Mycobacterium tuberculosis H37Rv adhC	52.2	74.9	343	NADP-dependent alcohol dehydrogenase
371	3871	348952	348098	855	sp RFBA_SALAN	Salmonella anatum M32 rfbA	62.8	84.9	285	glucose-1-phosphate thymidylyltransferase
372	3872	350310	348952	1359	gp D78182_5	Streptococcus mutans rmlC	49.5	74.0	192	dTDP-4-keto-L-rhamnose reductase
373	3873	351443	350313	1131	sp RMLB_STRMU	Streptococcus mutans XC rmlB	61.8	83.4	343	dTDP-glucose 4,6-dehydratase
374	3874	351948	351370	579	sp NOX_THETH	Thermus aquaticus HB8 nox	35.4	61.2	206	NADH dehydrogenase
375	3875	352693	353637	945	prf 2510361A	Staphylococcus aureus sirA	33.2	66.5	325	Fe regulated protein
376	3876	354387	353749	639						
377	3877	355906	354599	1308	sp Y17M_MYCTU	Mycobacterium tuberculosis H37Rv Rv3630	37.4	68.3	423	hypothetical membrane protein
378	3878	357229	355849	1380	gp SC5F2A_19	Streptomyces coelicolor SC5F2A.19c	34.1	62.5	461	metallopeptidase
379	3879	359354	357237	2118	prf 2502226A	Sphingomonas capsulata	28.4	56.4	708	prolyl endopeptidase
380	3880	360334	359762	573						
381	3881	361905	360814	1092	gp SCF43_2	Streptomyces coelicolor A3(2)	26.0	46.0	258	hypothetical membrane protein
382	3882	363151	362057	1095	gsp W56155	Corynebacterium ammoniagenes ATCC 6872	50.7	76.6	363	cell surface layer protein
383	3883	363824	365257	1434	prf 2404346B	Acinetobacter johnsonii ptk	28.5	57.2	453	autophosphorylating protein Tyr kinase
384	3884	365250	365852	603	prf 2404346A	Acinetobacter johnsonii ptp	39.2	68.6	102	protein phosphatase
385	3885	365855	366838	984						
386	3886	366832	368643	1812	sp CAPD_STAAU	Staphylococcus aureus M capD	33.0	65.7	613	capsular polysaccharide biosynthesis
387	3887	368642	367701	942	PRF 2109288X	Vibrio cholerae	41.0	51.0	90	ORF 3
388	3888	368647	369801	1155	prf 2423410L	Campylobacter jejuni wlaK	37.1	68.3	394	lipopolysaccharide biosynthesis / aminotransferase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
389	3889	369794	370405	612	gp AF014804_1	Neisseria meningitidis pglB	54.6	75.0	196	pilin glycosylation protein
390	3890	370613	371773	1161	sp CAPM_STAAU	Staphylococcus aureus M capM	33.4	69.2	380	capsular polysaccharide biosynthesis
391	3891	371929	373419	1491	pir S67859	Xanthomonas campestris gumJ	34.3	69.8	504	lipopolysaccharide biosynthesis / export protein
392	3892	373500	374813	1314	sp MURA_ENTCL	Enterobacter cloacae murA	31.4	64.6	427	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
393	3893	374833	375837	1005	sp MURB_BACSU	Bacillus subtilis murB	34.8	68.5	273	UDP-N-acetylenolpyruvoylglucosamine reductase
394	3894	375842	376876	1035	gp VCLPSS_9	Vibrio cholerae ORF39x2	32.0	57.3	356	sugar transferase
395	3895	377683	377832	150	prf 2211295A	Corynebacterium glutamicum	60.4	79.3	53	transposase
396	3896	378093	378227	135						
397	3897	378185	378511	327	pir S43613	Corynebacterium glutamicum ATCC 31831	75.7	94.3	70	transposase (insertion sequence IS31831)
398	3898	378562	378287	276						
399	3899	379837	378668	1170	pir G70539	Mycobacterium tuberculosis H37Rv Rv1565c	28.0	57.4	404	hypothetical protein
400	3900	380842	379850	993	gsp W37352	Pseudomonas aeruginosa PAO1 psbC	34.5	60.2	354	acetyltransferase
401	3901	381265	381495	231	PIR S60890	Corynebacterium glutamicum	44.0	53.0	65	hypothetical protein B
402	3902	381948	383108	1161	sp UDG8_ECOLI	Escherichia coli ugd	63.7	89.7	388	UDP-glucose 6-dehydrogenase
403	3903	383768	383496	273						
404	3904	385190	383982	1209						
405	3905	386195	385374	822	gp AF172324_3	Escherichia coli wbnA	32.1	65.0	243	glycosyl transferase
406	3906	386556	387200	645	gp AB008376_13	Escherichia coli 0157 wbhH	33.0	62.0	221	acetyltransferase
407	3907	387657	387463	195						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
408	3908	387692	389098	1407	gp CGLPD_1	Corynebacterium glutamicum ATCC 13032 lpd	99.6	100.0	469	dihydrolipoamide dehydrogenase
409	3909	389248	390168	921	pir JC4985	Xanthomonas campestris	41.7	68.1	295	UTP--glucose-1-phosphate uridylyltransferase
410	3910	390233	390730	498	gp PAU49666_2	Pseudomonas aeruginosa PAO1 orfX	43.8	71.9	153	regulatory protein
411	3911	392208	390787	1422	pir E70828	Mycobacterium tuberculosis H37Rv Rv0465c	57.0	81.3	477	transcriptional regulator
412	3912	392705	393475	771	gp SCM10_12	Streptomyces coelicolor A3(2) SCM10.12c	34.8	67.4	230	cytochrome b subunit
413	3913	393639	395513	1875	pir A27763	Bacillus subtilis sdhA	32.4	61.2	608	succinate dehydrogenase flavoprotein
414	3914	395426	396262	837	gp BMSDHCAB_4	Paenibacillus macerans sdhB	27.5	56.2	258	succinate dehydrogenase subunit B
415	3915	396315	396650	336						
416	3916	396672	396932	261						
417	3917	397040	396411	630						
418	3918	397730	397825	96						
419	3919	397884	398222	339						
420	3920	398206	397232	975	gp SCC78_5	Streptomyces coelicolor SCC78.05	26.3	49.8	259	hypothetical protein
421	3921	398329	399579	1251	sp YJIN_ECOLI	Escherichia coli K12 yjiN	32.7	64.3	431	hypothetical protein
422	3922	399598	400017	420						
423	3923	400039	400341	303						
424	3924	400473	401150	678	sp TCMR_STRGA	Streptomyces glaucescens GLA.0 tcmR	26.4	53.8	197	tetracenomycin C transcription repressor
425	3925	401050	401253	204						
426	3926	401150	402796	1647	gp AF164961_8	Streptomyces fradiae T#2717 urdJ	36.1	74.6	499	transporter

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
427	3927	402799	404430	1632	gp AF1b4961_8	Streptomyces fradiae T#2717 urdJ	39.6	74.6	508	transporter
428	3928	405410	404508	912	sp PURU_CORSP	Corynebacterium sp. P-1 purU	40.9	72.7	286	formyltetrahydrofolate deformylase
429	3929	405480	406145	666	sp DEOC_BACSU	Bacillus subtilis deoC	38.5	74.0	208	deoxyribose-phosphate aldolase
430	3930	406310	406161	150						
431	3931	406417	405521	897						
432	3932	406550	407416	867	prf 2413441K	Mycobacterium avium GIR10 mav346	26.8	53.6	280	hypothetical protein
433	3933	407708	407409	300	pir A70907	Mycobacterium tuberculosis H37Rv Rv0190	58.7	85.9	92	hypothetical protein
434	3934	408546	409145	600						
435	3935	409975	407711	2265	sp CTPB_MYCLE	Mycobacterium leprae ctpB	45.7	75.3	748	cation-transporting P-type ATPase B
436	3936	410476	410027	450						
437	3937	410683	412545	1863	sp AMYH_YEAST	Saccharomyces cerevisiae S288C YIR019C sta1	27.3	56.1	626	glucan 1,4-alpha-glucosidase
438	3938	412557	413633	1077	gp AF109162_1	Corynebacterium diphtheriae hmuT	57.2	83.6	348	hemin-binding periplasmic protein
439	3939	413643	414710	1068	gp AF109162_2	Corynebacterium diphtheriae hmuU	65.2	90.3	330	ABC transporter
440	3940	414714	415526	813	gp AF109162_3	Corynebacterium diphtheriae hmuV	63.8	85.0	254	ABC transporter ATP-binding protein
441	3941	415643	416599	957	gp SCC75A_17	Streptomyces coelicolor C75A SCC75A.17c	28.6	56.4	266	hypothetical protein
442	3942	416603	417439	837	gp SCC75A_17	Streptomyces coelicolor C75A SCC75A.17c	32.6	61.6	258	hypothetical protein
443	3943	418354	417545	810						
444	3944	419253	418441	813						
445	3945	419757	419257	501						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
446	3946	419785	420885	1101	gp ECOMURBA_1	Escherichia coli RDD012 murB	30 1	58 4	356	UDP-N-acetylpyruvoylglucosamine reductase
447	3947	420866	421516	651						
448	3948	421043	420309	735						
449	3949	421858	422031	174						
450	3950	423793	422090	1704	sp LCFA_BACSU	Bacillus subtilis lcfA	35.5	68 1	558	long-chain-fatty-acid--CoA ligase
451	3951	423878	425131	1254	gp SC2G5_6	Streptomyces coelicolor SC2G5 06	33.9	58 7	416	transferase
452	3952	425177	425920	744	sp PMGY_STRCO	Streptomyces coelicolor A3(2) gpm	70 7	84 2	246	phosphoglycerate mutase
453	3953	425934	427172	1239	prf 2404434A	Mycobacterium bovis senX3	49 2	74 8	417	two-component system sensor histidine kinase
454	3954	427172	427867	696	prf 2404434B	Mycobacterium bovis BCG regX3	75 8	90 9	231	two-component response regulator
455	3955	428561	429439	879						
456	3956	432023	429438	2586	gp SCE25_30	Streptomyces coelicolor A3(2) SCE25 30	31.3	60 7	921	ABC transporter ATP-binding protein
457	3957	433028	432126	903	sp YV21_MYCTU	Mycobacterium tuberculosis H37Rv RV3121	45 0	66 9	269	cytochrome P450
458	3958	433062	433988	927	prf 2512277A	Pseudomonas aeruginosa ppx	28 8	57 8	306	exopolyphosphatase
459	3959	434010	434822	813	sp YV23_MYCTU	Mycobacterium tuberculosis H37Rv Rv0497	28 8	57 3	302	hypothetical membrane protein
460	3960	434886	435695	810	sp PROC_CORGL	Corynebacterium glutamicum ATCC 17965 proC	100 0	100 0	269	pyrroline-5-carboxylate reductase
461	3961	434986	433865	1122	gp D88733_1	Equine herpesvirus 1 ORF71	25 4	52 0	394	membrane glycoprotein
462	3962	435940	436137	198	pir S72921	Mycobacterium leprae B2168_C1_172	76 4	94 6	55	hypothetical protein
463	3963	436321	436103	219						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
464	3964	436463	436561	99	gp SCE68_25	Streptomyces coelicolor SCE68 25c	89.7	100.0	29	hypothetical protein
465	3965	436573	436764	192						
466	3966	437233	437850	618						
467	3967	438044	436980	1065	pir S72914	Mycobacterium leprae MTCY20G9.32C serB	51.0	77.4	296	phosphoserine phosphatase
468	3968	438179	438424	246	sp YV35_MYCTU	Mycobacterium tuberculosis H37Rv Rv0508	40.5	66.2	74	hypothetical protein
469	3969	438294	438037	258						
470	3970	438516	439904	1389	sp HEM1_MYCLE	Mycobacterium leprae hemA	44.4	74.3	455	glutamyl-tRNA reductase
471	3971	439909	440814	906	pir S72887	Mycobacterium leprae hem3b	50.7	75.3	308	hydroxymethylbilane synthase
472	3972	441220	441591	372						
473	3973	442482	441501	882	sp CATM_ACICA	Acinetobacter calcoaceticus catM	27.1	57.6	321	cat operon transcriptional regulator
474	3974	442758	444158	1401	sp SHIA_ECOLI	Escherichia coli K12 shiA	35.5	72.2	417	shikimate transport protein
475	3975	444185	446038	1854	sp 3SHD_NEUCR	Neurospora crassa qa4	28.2	57.9	309	3-dehydroshikimate dehydratase
476	3976	446538	447386	849	gp AF124518_2	Corynebacterium glutamicum ASO19 aroE	98.2	98.6	282	shikimate dehydrogenase
477	3977	447670	447398	273						
478	3978	449179	448130	1050	sp POTG_ECOLI	Escherichia coli K12 potG	34.7	68.6	363	putrescine transport protein
479	3979	449714	449100	615						
480	3980	450826	449183	1644	sp SFUB_SERMA	Serratia marcescens sfuB	25.1	55.2	578	iron(III)-transport system permease protein
481	3981	450849	451961	1113						
482	3982	451895	450837	1059	gp SHU75349_1	Brachyspira hyodysenteriae bitA	25.1	59.9	347	periplasmic-iron-binding protein
483	3983	452661	454430	1770	pir S72909	Mycobacterium leprae cysG	46.5	71.6	486	uroporphyrin-III C-methyltransferase
484	3984	454450	454875	426						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	In tial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
485	3985	454967	455983	1017	sp HEM2_STRCO	Streptomyces coelicolor A3(2) hemB	60 8	83 1	337	delta-aminolevulinic acid dehydratase
486	3986	456016	456597	582						
487	3987	456641	457150	510						
488	3988	457357	459900	2544	sp CTPB_MYCLE	Mycobacterium leprae ctpB	27.4	56.5	858	cation-transporting P-type ATPase B
489	3989	459425	458583	843						
490	3990	460020	461093	1074	sp DCUP_STRCO	Streptomyces coelicolor A3(2) hemE	55 0	76 7	364	uroporphyrinogen decarboxylase
491	3991	461112	462455	1344	sp PPOX_BACSU	Bacillus subtilis hemY	28 0	59 9	464	protoporphyrinogen IX oxidase
492	3992	462557	463867	1311	sp GSA_MYCLE	Mycobacterium leprae hemI	61 7	83 5	425	glutamate-1-semialdehyde 2,1-aminomutase
493	3993	463867	464472	606	sp PMG2_ECOLI	Escherichia coi K12 gpmB	28 0	52 7	161	phosphoglycerate mutase
494	3994	464482	465102	621	pir A70545	Mycobacterium tuberculosis H37Rv Rv0526	44 7	71.2	208	hypothetical protein
495	3995	465118	465909	792	pir B70545	Mycobacterium tuberculosis H37Rv ccsA	53 5	85 3	245	cytochrome c-type biogenesis protein
496	3996	465949	467571	1623	pir C70545	Mycobacterium tuberculosis H37Rv Rv0528	50 7	76 0	533	hypothetical membrane protein
497	3997	467648	468658	1011	pir D70545	Mycobacterium tuberculosis H37Rv ccsB	44 1	77 8	338	cytochrome c biogenesis protein
498	3998	469370	470170	801						
499	3999	470184	470654	471	pir G70790	Mycobacterium tuberculosis H37Rv Rv3678c pb5	38 9	69 4	144	transcriptional regulator
500	4000	471013	470657	357	prf 2420312A	Staphylococcus aureus zntR	31 1	72 2	90	Zn/Co transport repressor
501	4001	471420	471121	300						
502	4002	471515	471847	333	pir F70545	Mycobacterium tuberculosis H37Rv Rv0531	39 0	78 1	82	hypothetical membrane protein
503	4003	472808	471915	894	sp MENA_ECOLI	Escherichia coli K12 menA	33 6	61 5	301	1,4-dihydroxy-2-naphthoate octaprenyltransferase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
504	4004	472946	473811	864	gp AF125164_6	Bacteroides fragilis wcgB	32 4	62 6	238	glycosyl transferase
505	4005	475136	473814	1323	prf 2423270B	Rhizobium trifolii matB	25 4	51 5	421	malonyl-CoA-decarboxylase
506	4006	475407	474997	411	sp YQJF_ECOLI	Escherichia coli K12 yqjF	35 3	65 5	139	hypothetical membrane protein
507	4007	477048	475489	1560	pir S27612	Pseudomonas putida	50.4	76 0	520	ketoglutarate semialdehyce dehydrogenase
508	4008	477995	477048	948	sp KDGD_PSEPU	Pseudomonas putida KDGDH	48 5	75.6	303	5-dehydro-4-deoxyglucarate dehydratase
509	4009	478970	478092	879	sp ALSR_BACSU	Bacillus subtilis 168 alsR	36 9	66.2	293	als operon regulatory protein
510	4010	479303	478989	315	pir B70547	Mycobacterium tuberculosis H37Rv Rv0543c	33.0	64 9	94	hypothetical protein
511	4011	480154	480597	444						
512	4012	480201	479452	750	gp SSP277295_9	Sphingomonas sp LB126 fldB	28.1	54 7	267	2-pyrone-4,6-dicarboxylic acid
513	4013	480624	480208	417						
514	4014	481001	480624	378						
515	4015	481391	481131	261						
516	4016	482668	481394	1275	pir D70547	Mycobacterium tuberculosis H37Rv pitA	60.0	83 2	410	low-affinity inorganic phosphate transporter
517	4017	483587	483366	222						
518	4018	483942	483637	306						
519	4019	485062	484106	957	sp MENB_BACSU	Bacillus subtilis menB	48 5	70 3	293	naphthoate synthase
520	4020	485384	485985	603	gp AE001957_12	Deinococcus radiodurans DR1070	57 9	82 7	202	peptidase E
521	4021	485385	485077	309	pir C70304	Aquifex aeolicus VF5 phhB	37 7	68.8	77	pterin-4a-carbinolamine dehydratase
522	4022	486001	487014	1014	pir D70548	Mycobacterium tuberculosis H37Rv Rv0553 menC	54.0	76.7	335	muconate cycloisomerase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
523	4023	487028	488656	1629	sp MEND_BACSU	Bacillus subtilis menD	29.4	54.9	606	2-oxoglutarate decarboxylase and 2-succinyl-6-hydroxy-2,4-cyclohexadiene 1 carboxylate synthase
524	4024	488660	489100	441	pir G70548	Mycobacterium tuberculosis H37Rv Rv0556	37.2	64.9	148	hypothetical membrane protein
525	4025	489209	490447	1239	pir H70548	Mycobacterium tuberculosis H37Rv pimB	22.8	54.2	408	alpha-D-mannose-alpha(1-6)phosphatidyl myo-inositol monomannoside transferase
526	4026	490580	491938	1359	sp CYCA_ECOLI	Escherichia coli K12 cycA	66.2	89.9	447	D-serine/D-alanine/glycine transporter
527	4027	491966	492655	690	sp UBIE_ECOLI	Escherichia coli K12 ubiE	37.1	66.7	237	ubiquinone/menaquinone biosynthesis methyltransferase
528	4028	492915	493583	669						
529	4029	493916	492645	1272	pir D70549	Mycobacterium tuberculosis H37Rv Rv0561c	49.0	76.7	412	oxidoreductase
530	4030	494061	495110	1050	sp HEP2_BACST	Bacillus stearothermophilus ATCC 10149 hep1	39.2	67.1	316	heptaprenyl diphosphate synthase component II
531	4031	496810	497142	333	gp AF130462_2	Corynebacterium glutamicum ATCC 13032 secE	100.0	100.0	111	preprotein translocase SecE subunit
532	4032	497374	498327	954	gp AF130462_3	Corynebacterium glutamicum ATCC 13032 nusG	100.0	100.0	318	transcriptional antiterminator protein
533	4033	498598	499032	435	gp AF130462_4	Corynebacterium glutamicum ATCC 13032 rplK	100.0	100.0	145	50S ribosomal protein L11
534	4034	499162	499869	708	gp AF130462_5	Corynebacterium glutamicum ATCC 13032 rplA	100.0	100.0	236	50S ribosomal protein L1
535	4035	501436	499925	1512	gp SC5H4_2	Streptomyces coelicolor SC5H4.02	23.1	50.2	564	regulatory protein
536	4036	501577	502920	1344	sp GABT_MYCTU	Mycobacterium tuberculosis H37Rv RV2589 gabT	60.5	82.4	443	4-aminobutyrate aminotransferase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	nitial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
537	4037	502925	504283	1359	sp GABD_ECOLI	Escherichia coli K12 gabD	40.8	71.8	461	succinate-semialdehyde dehydrogenase (NAD(P)+)
538	4038	503739	503272	468	GP ABCARRA_2	Azospirillum brasilense carR	32.0	38.0	150	novel two-component regulatory system
539	4039	504379	505569	1191	sp TYRP_ECOLI	Escherichia coli K12 o341#7 tyrP	25.5	49.9	447	tyrosine-specific transport protein
540	4040	505698	507647	1950	sp CTPG_MYCTU	Mycobacterium tuberculosis H37Rv RV1992C ctpG	33.2	64.4	615	cation-transporting ATPase G
541	4041	507669	509081	1413	sp P49_STRLI	Streptomyces lividans P49	40.2	66.2	468	hypothetical protein or dehydrogenase
542	4042	509094	509696	603						
543	4043	509998	510510	513	sp RL10_STRGR	Streptomyces griseus N2-3-11 rplJ	52.9	84.7	170	50S ribosomal protein L10
544	4044	510591	510974	384	sp RL7_MYCTU	Mycobacterium tuberculosis H37Rv RV0652 rplL	72.3	89.2	130	50S ribosomal protein L7/L12
545	4045	511126	510989	138						
546	4046	511536	512507	972	p r A70962	Mycobacterium tuberculosis H37Rv Rv0227c	25.8	55.5	283	hypothetical membrane protein
547	4047	512913	516407	3495	sp RPOB_MYCTU	Mycobacterium tuberculosis H37Rv RV0667 rpoB	75.4	90.4	1180	DNA-directed RNA polymerase beta chain
548	4048	516494	520492	3999	sp RPOC_MYCTU	Mycobacterium tuberculosis H37Rv RV0668 rpoC	72.9	88.7	1332	DNA-directed RNA polymerase beta chain
549	4049	519277	518696	582	GP AF121004_1	Mycobacterium tuberculosis H37Rv Rv0166c	39.0	52.0	169	hypothetical protein
550	4050	520671	520850	180						
551	4051	520865	521644	780	gp SCJ9A_15	Streptomyces coelicolor A3(2) SCJ9A 15c	39.2	63.8	232	DNA-binding protein
552	4052	522476	521679	798	sp YT08_MYCTU	Mycobacterium tuberculosis H37Rv RV2908C	29.3	57.7	215	hypothetical protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Termina (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
553	4053	522804	523059	366	sp RS12_MYCIT	Mycobacterium intracellulare rpsL	90.9	97.5	121	30S ribosomal protein S12
554	4054	523069	523533	465	sp RS7_MYCSM	Mycobacterium smegmatis LR222 rpsG	81.8	94.8	154	30S ribosomal protein S7
555	4055	523896	526010	2115	sp EFG_MICLU	Micrococcus luteus fusA	71.7	88.9	709	elongation factor G
556	4056	526070	523911	2160						
557	4057	526156	526013	144						
558	4058	527121	526894	228	GSP Y37841	Chlamydia trachomatis	56.0	78.0	44	lipoprotein
559	4059	527759	527607	153						
560	4060	528040	528768	729						
561	4061	529570	528779	792	sp FEPC_ECOLI	Escherichia coli K12 fepC	56.2	83.7	258	ferric enterobactin transport ATP-binding protein
562	4062	530626	529592	1035	sp FEPG_ECOLI	Escherichia coli K12 fepG	45.6	77.8	329	ferric enterobactin transport protein
563	4063	531782	530748	1035	sp FEPD_ECOLI	Escherichia coli K12 fepD	48.1	80.6	335	ferric enterobactin transport protein
564	4064	532008	532523	516	gp CTACTAGEN_1	Thermoanaerobacterium thermosaccharolyticum actA	56.6	79.3	145	butyryl-CoA acetate coenzyme A transferase
565	4065	533099	533401	303	sp RS10_PLARO	Planobispora rosea ATCC 53733 rpsJ	84.2	99.0	101	30S ribosomal protein S10
566	4066	533437	534090	654	sp RL3_MYCBO	Mycobacterium bovis BCG rplC	66.5	89.6	212	50S ribosomal protein L3
567	4067	534087	533401	687						
568	4068	534090	534743	654	sp RL4_MYCBO	Mycobacterium bovis BCG rplD	71.2	90.1	212	50S ribosomal protein L4
569	4069	534746	535048	303	sp RL23_MYCBO	Mycobacterium bovis BCG rplW	74.0	90.6	96	50S ribosomal protein L23
570	4070	535072	534746	327						
571	4071	535079	535915	840	sp RL2_MYCLE	Mycobacterium bovis BCG rplB	80.7	92.9	280	50S ribosomal protein L2
572	4072	535935	536210	276	sp RS19_MYCTU	Mycobacterium tuberculosis H37Rv Rv0705 rpsS	87.0	98.9	92	30S ribosomal protein S19
573	4073	536183	535899	285						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a)	Function
574	4074	536217	536576	360	sp RL22_MYCTU	Mycobacterium tuberculosis H37Rv Rv0706 rplV	74.3	91.7	109	50S ribosomal protein L22
575	4075	536579	537322	744	sp RS3_MYCBO	Mycobacterium bovis BCG rpsC	77.4	91.2	239	30S ribosomal protein S3
576	4076	537328	537741	414	sp RL16_MYCBO	Mycobacterium bovis BCG rplP	69.3	88.3	137	50S ribosomal protein L16
577	4077	537744	537971	228	sp RL29_MYCBO	Mycobacterium bovis BCG rpmC	65.7	88.1	67	50S ribosomal protein L29
578	4078	537977	538252	276	sp RS17_MYCBO	Mycobacterium bovis BCG rpsQ	69.5	89.0	82	30S ribosomal protein S17
579	4079	538267	537974	294						
580	4080	538698	538381	318						
581	4081	539413	538718	696						
582	4082	539741	540106	366	sp RL14_MYCTU	Mycobacterium tuberculosis H37Rv Rv0714 rplN	83.6	95.1	122	50S ribosomal protein L14
583	4083	540112	540423	312	sp RL24_MYCTU	Mycobacterium tuberculosis H37Rv Rv0715 rplX	75.2	91.4	105	50S ribosomal protein L24
584	4084	540426	540998	573	sp RL5_MICLU	Micrococcus luteus rplE	73.6	92.3	183	50S ribosomal protein L5
585	4085	541048	542079	1032						
586	4086	542896	542090	807	sp 2DKG_CORSP	Corynebacterium sp.	52.3	74.2	260	2,5-diketo-D-gluconic acid reductase
587	4087	543412	542921	492						
588	4088	544329	543415	915	sp FDHD_WOLSU	Wolinella succinogenes fdhD	28.9	59.7	298	formate dehydrogenase chain D
589	4089	544670	544335	336	gp SCGD3_29	Streptomyces coelicolor A3(2) SCGD3.29c	37.2	68.1	94	molybdopterin-guanine dinucleotide biosynthesis protein
590	4090	546889	544757	2133	sp FDHF_ECOLI	Escherichia coli fdfF	24.3	53.4	756	formate dehydrogenase H or alpha chain
591	4091	547329	548084	756						
592	4092	548990	548187	804						
593	4093	550651	548990	1662	sp YC81_MYCTU	Mycobacterium tuberculosis H37Rv Rv1281c oppD	26.9	52.6	524	ABC transporter ATP binding protein
594	4094	551844	550699	1146						
595	4095	552927	551854	1074						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
596	4096	554129	552948	1182	pir E69424	Archaeoglobus fulgidus AF1398	24.7	50.4	405	hypothetical protein
597	4097	554919	554452	468	gp AE001931_13	Deinococcus radiodurans DR0763	42.7	66.7	150	hypothetical protein
598	4098	555331	555726	396	pir S29885	Micrococcus luteus	75.8	97.7	132	30S ribosomal protein S8
599	4099	555749	556282	534	pir S29886	Micrococcus luteus	59.2	87.7	179	50S ribosomal protein L6
600	4100	556289	556690	402	sp RL18_MICLU	Micrococcus luteus rplR	67.3	90.9	110	50S ribosomal protein L18
601	4101	556734	557366	633	sp RS5_MICLU	Micrococcus luteus rpsE	67.8	88.3	171	30S ribosomal protein S5
602	4102	557373	557555	183	sp RL30_ECOLI	Escherichia coli K12 rpmJ	54.6	76.4	55	50S ribosomal protein L30
603	4103	557565	558008	444	sp RL15_MICLU	Micrococcus luteus rplO	66.4	87.4	143	50S ribosomal protein L15
604	4104	557588	556860	729						
605	4105	558517	558197	321	prf 2204281A	Streptomyces coelicolor msdA	46.9	68.8	128	methylmalonic acid semialdehyde dehydrogenase
606	4106	558969	558607	363						
607	4107	559805	560260	456	GP ABCARRA_2	Azospirillum brasilense carR	47.0	52.0	125	novel two-component regulatory system
608	4108	560634	559144	1491	prf 2516399E	Rhodococcus rhodochrous plasmid pRTL1 orf5	41.7	71.5	487	aldehyde dehydrogenase or betaine aldehyde dehydrogenase
609	4109	561368	560634	735						
610	4110	562632	562937	306						
611	4111	562633	561368	1266	prf 2411257B	Sphingomonas sp recA2	41.1	71.6	409	reductase
612	4112	562963	562646	318	prf 2313248B	Rhodobacter capsulatus fdxE	47.7	66.4	107	2Fe2S ferredoxin
613	4113	563736	562993	744	gp PPU24215_2	Pseudomonas putida cymB	35.8	70.8	257	p-cumic alcohol dehydrogenase
614	4114	563871	564083	213	PIR H72754	Aeropyrum pernix K1 APE0029	50.0	56.0	50	hypothetical protein
615	4115	565471	563732	1740	pir JC4176	Pyrococcus furiosus Vc1 DSM 3638 ppsA	22.9	45.0	629	phosphoenolpyruvate synthetase
616	4116	566759	565680	1080	pir JC4176	Pyrococcus furiosus Vc1 DSM 3638 ppsA	38.6	66.7	378	phosphoenolpyruvate synthetase
617	4117	568088	566799	1290	prf 2104333G	Rhodococcus erythropolis thcB	34.8	65.2	422	cytochrome P450

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
618	4118	569075	568272	804	prf 2512309A	Erwinia carotovora carotovora kdgR	28.5	66.0	256	transcriptional repressor
619	4119	570774	571316	543	sp KAD_MICLU	Micrococcus luteus adk	48.9	81.0	184	adenylate kinase
620	4120	571367	570756	612						
621	4121	571476	572267	792	sp AMPM_BACSU	Bacillus subtilis 168 map	43.1	74.7	253	methionine aminopeptidase
622	4122	572349	573176	828						
623	4123	573407	573622	216	pir F69644	Bacillus subtilis infA	77.0	86.0	72	translation initiation factor IF-1
624	4124	573816	574181	366	prf 2505353B	Thermus thermophilus HB8 rps13	66.4	91.0	122	30S ribosomal protein S13
625	4125	574187	574588	402	sp RS11_STRCO	Streptomyces coelicolor A3(2) SC6G4.06 rpsK	81.3	93.3	134	30S ribosomal protein S11
626	4126	574615	575217	603	prf 2211287I	Mycobacterium tuberculosis H37Rv RV3458C rpsD	82.6	93.9	132	30S ribosomal protein S4
627	4127	575338	576351	1014	sp RPOA_BACSU	Bacillus subtilis 168 rpoA	51.1	77.8	311	RNA polymerase alpha subunit
628	4128	575366	575211	156						
629	4129	576410	576898	489	sp RL17_ECOLI	Escherichia coli K12 rplQ	51.6	77.1	122	50S ribosomal protein L17
630	4130	577057	577923	867	sp TRUA_ECOLI	Escherichia coli K12 truA	37.0	61.1	265	pseudouridylate synthase A
631	4131	578033	580429	2397	pir G70695	Mycobacterium tuberculosis H37Rv Rv3779	24.8	51.2	786	hypothetical membrane protein
632	4132	580891	580436	456						
633	4133	581221	580919	303						
634	4134	581406	582862	1257	pir A70836	Mycobacterium tuberculosis H37Rv Rv0283	27.4	53.8	485	hypothetical protein
635	4135	582684	584228	1545	sp DIM_ARATH	Arabidopsis thaliana CV DIM	22.8	50.9	505	cell elongation protein
636	4136	584268	585620	1353	sp CFA_ECOLI	Escherichia coli K12 cfa	30.7	56.0	423	cyclopropane fatty acyl-phospholipid synthase
637	4137	585823	586248	426	gp SCL2_30	Streptomyces coelicolor A3(2) SCL2.30c	28.0	59.0	100	hypothetical membrane protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
638	4138	587757	586399	1359	sp ELYA_BACAO	Bacillus alcalophilus	31 3	58 0	273	high-alkaline serine proteinase
639	4139	589015	587645	1371	pir T10930	Streptomyces coelicolor A3(2) SC3C3.21	24 0	50 6	516	hypothetical membrane protein
640	4140	589296	592862	3567	pir E70977	Mycobacterium tuberculosis H37Rv Rv3447c	65 0	38 4	1260	hypothetical membrane protein
641	4141	590411	589590	822						
642	4142	590560	589898	663						
643	4143	592862	593761	900						
644	4144	593935	594258	324	pir C70977	Mycobacterium tuberculosis H37Rv Rv3445c	31.1	69 9	103	hypothetical protein
645	4145	594293	594580	288	prf 2111376A	Mycobacterium tuberculosis	36 3	81 3	80	early secretory antigen target ESAT 6 protein
646	4146	594939	595379	441	sp RL13_STRCO	Streptomyces coelicolor A3(2) SC6G4.12. rplM	58 6	82 1	145	50S ribosomal protein L13
647	4147	595382	595927	546	sp RS9_STRCO	Streptomyces coelicolor A3(2) SC6G4.13. rpsI	49 2	72 4	181	30S ribosomal protein S9
648	4148	596109	597449	1341	prf 2320260A	Staphylococcus aureus femR315	48 9	76 4	450	phosphoglucosamine mutase
649	4149	597892	598194	303						
650	4150	598194	599702	1509	pir S75138	Synechocystis sp. PCC6803 slr1753	29 3	45 6	318	hypothetical protein
651	4151	599350	598778	573						
652	4152	599699	599932	234						
653	4153	600876	600022	855	pir S73000	Mycobacterium leprae B229. F1. 20	44 0	72 2	259	hypothetical protein
654	4154	600971	602053	1083	sp ALR_MYCTU	Mycobacterium tuberculosis H37Rv RV3423C alr	41 6	68 5	368	alanine racemase
655	4155	602080	602574	495	sp Y097_MYCTU	Mycobacterium tuberculosis H37Rv Rv3422c	48.7	78 6	154	hypothetical protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
656	4156	602811	604409	1599	sp YIDE_ECOLI	Escherichia coli K12 yidE	28.9	66.2	550	hypothetical membrane protein
657	4157	604470	605708	1239	gp PSJ00161_1	Propionibacterium shermanii pip	51.3	77.6	411	proline iminopeptidase
658	4158	605718	606392	675	sp Y098_MYCTU	Mycobacterium tuberculosis H37Rv Rv3421c	52.2	75.4	207	hypothetical protein
659	4159	606392	606898	507	sp RIMI_ECOLI	Escherichia coli K12 rimI	30.3	59.9	132	ribosomal-protein-alanine N-acetyltransferase
660	4160	606905	607936	1032	sp GCP_PASHA	Pasteurella haemolytica SEROTYPE A1 gcp	46.1	75.2	319	O-sialoglycoprotein endopeptidase
661	4161	607958	609679	1722	sp Y115_MYCTU	Mycobacterium tuberculosis H37Rv Rv3433c	38.4	59.4	571	hypothetical protein
662	4162	609747	610175	429						
663	4163	610268	609816	453						
664	4164	610348	610644	297	sp CH10_MYCTU	Mycobacterium tuberculosis H37Rv RV3418C mopB	76.0	94.0	100	heat shock protein groES
665	4165	610659	612272	1614	sp CH61_MYCLE	Mycobacterium leprae B229_C3_248 groE1	63.3	85.1	537	heat shock protein groEL
666	4166	611200	610946	255	GP MSGTCWPA_1	Mycobacterium tuberculosis	50.0	56.0	76	hypothetical protein
667	4167	612266	611109	1158	GP MSGTCWPA_3	Mycobacterium tuberculosis	34.0	45.0	138	hypothetical protein
668	4168	612714	612418	297	gp AF073300_1	Mycobacterium smegmatis whiB3	64.9	88.3	94	regulatory protein
669	4169	613156	613719	564	sp Y09F_MYCTU	Mycobacterium tuberculosis H37Rv Rv3414c sigD	55.2	81.6	174	RNA polymerase sigma factor
670	4170	613722	614747	1026						
671	4171	615180	614803	378	sp Y09H_MYCLE	Mycobacterium leprae B1620_F3_131	41.4	69.8	116	hypothetical protein
672	4172	615336	616853	1518	gp AB003154_1	Corynebacterium ammoniagenes ATCC 6872 guaB	80.8	93.9	504	IMP dehydrogenase
673	4173	616231	615605	627	PIR F71456	Pyrococcus horikoshii PH0308	39.0	53.0	146	hypothetical protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (aa)	Function
674	4174	616973	618094	1122	gp AB003154_2	Corynebacterium ammoniagenes ATCC 6872	70.9	86.1	381	IMP dehydrogenase
675	4175	619013	618093	921	sp YBIF_ECOLI	Escherichia coli K12 ybiF	38.0	67.5	274	hypothetical membrane protein
676	4176	619086	619994	909	prf 1516239A	Bacillus subtilis gltC	29.0	58.4	262	glutamate synthetase positive regulator
677	4177	620004	621572	1569	sp GUAA_CORAM	Corynebacterium ammoniagenes guaA	81.6	92.8	517	GMP synthetase
678	4178	620926	620264	663						
679	4179	621717	622157	441						
680	4180	622269	622457	189						
681	4181	623635	622460	1176	gp SCD63_22	Streptomyces coelicolor A3(2)	20.5	39.6	513	hypothetical membrane protein
682	4182	623800	624939	1140	gp SC6E10_15	Streptomyces coelicolor A3(2) SC6E10.15c	26.8	48.7	411	two-component system sensor histidine kinase
683	4183	624985	625674	690	sp DEGU_BACSU	Bacillus subtilis 168 degU	33.5	65.1	218	transcriptional regulator or extracellular proteinase response regulator
684	4184	625677	626000	324						
685	4185	626558	626070	489						
686	4186	627539	626577	963						
687	4187	627727	628551	825	pir B70975	Mycobacterium tuberculosis H37Rv Rv3395c	30.9	64.2	201	hypothetical protein
688	4188	628551	630140	1590	pir A70975	Mycobacterium tuberculosis H37Rv Rv3394c	37.5	64.1	563	hypothetical protein
689	4189	630810	630151	660						
690	4190	630949	631809	861	gp SC5B8_20	Streptomyces coelicolor A3(2) SC5B8.20c	33.8	62.9	275	hypothetical protein
691	4191	632684	631824	861	gp AE001935_7	Deinococcus radiodurans DR0809	27.8	58.3	288	hypothetical membrane protein
692	4192	633079	632690	390						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initia (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
693	4193	633474	633079	396	gp MMU92075_3	Mycobacterium marinum	36.8	67.4	95	hypothetical membrane protein
694	4194	635175	633532	1644	gp AF139916_3	Brevibacterium linens ATCC 9175 crtI	50.4	76.2	524	phytoene desaturase
695	4195	636089	635178	912	gp AF139916_2	Brevibacterium linens ATCC 9175 crtB	42.0	71.2	288	phytoene synthase
696	4196	638278	636089	2190	gp SCF43A_29	Streptomyces coelicolor A3(2) SCF43A.29c	48.6	75.6	722	transmembrane transport protein
697	4197	639462	638317	1146	gp AF139916_11	Brevibacterium linens crtE	32.7	63.8	367	geranylgeranyl pyrophosphate (GGPP) synthase
698	4198	639624	640208	585	gp AF139916_14	Brevibacterium linens	38.3	68.1	188	transcriptional regulator (MarR family)
699	4199	640879	640232	648	sp BLC_CITFR	Citrobacter freundii blc OS60 blc	33.1	62.1	145	outer membrane lipoprotein
700	4200	641133	642557	1425	gp AF139916_1	Brevibacterium linens	48.7	74.2	462	hypothetical protein
701	4201	643959	642556	1404	gp AF139916_5	Brevibacterium linens ATCC 9175 cpd1	40.0	63.2	497	DNA photolyase
702	4202	644826	644778	753	gp AF155804_7	Streptococcus suis cps1K	25.9	53.7	205	glycosyl transferase
703	4203	647590	645176	2415	gp SCE25_30	Streptomyces coelicolor A3(2) SCE25.30	24.3	54.9	897	ABC transporter
704	4204	648309	647593	717	prf 2420410P	Bacillus subtilis 168 yvrO	35.4	72.2	223	ABC transporter
705	4205	648467	648315	153						
706	4206	649105	648440	666	prf 2320284D	Helicobacter pylori abcD	35.9	75.2	206	ABC transporter
707	4207	649342	650187	846						
708	4208	650193	649114	1080	sp ABC_ECOLI	Escherichia coli TAP90 abc	43.6	75.4	346	ABC transporter
709	4209	651288	650392	897	sp HLPA_HAEIN	Haemophilus influenzae SEROTYPE B hlpA	28.7	67.2	268	lipoprotein
710	4210	651601	654612	3012	prf 2517386A	Thermus aquaticus dnaE	30.2	57.5	1101	DNA polymerase III
711	4211	654670	655122	447	gp SCE126_11	Streptomyces coelicolor A3(2) SCE126.11	41.5	62.3	159	hypothetical protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
712	4212	655122	656534	1413	gp SCE9_1	Streptomyces coelicolor A3(2) SCE9.01	26.1	56.0	468	hypothetical membrane protein
713	4213	655834	655097	738						
714	4214	656547	657215	669	pir C70884	Mycobacterium tuberculosis H37Rv Rv2788 sirR	50.3	76.4	203	transcriptional repressor
715	4215	658002	657205	798	gp SCG8A_5	Streptomyces coelicolor A3(2) SCG8A.05c	34.9	61.7	264	hypothetical protein
716	4216	658005	658142	138						
717	4217	658155	658928	774	pir C69459	Archaeoglobus fulgidus AF1676	42.5	71.8	245	transcriptional regulator (Sir2 family)
718	4218	658933	659424	492	gp SC5H1_34	Streptomyces coelicolor A3(2) SC5H1.34	45.2	78.3	157	hypothetical protein
719	4219	659543	660538	996	gp CDU02617_1	Corynebacterium diphtheriae irp1	31.1	62.2	357	iron-regulated lipoprotein precursor
720	4220	661120	660650	471	pir E70971	Mycobacterium tuberculosis H37Rv Rv3366 spoU	62.9	86.1	151	rRNA methylase
721	4221	661166	662017	852	pir C70970	Mycobacterium tuberculosis H37Rv Rv3356c folD	70.9	87.4	278	methylenetetrahydrofolate dehydrogenase
722	4222	662120	662374	255	gp MLCB1779_8	Mycobacterium leprae MLCB1779.16c	31.3	76.3	80	hypothetical membrane protein
723	4223	663761	662382	1380	gp SC66T3_18	Streptomyces coelicolor A3(2) SC66T3.18c	34.0	63.2	489	hypothetical protein
724	4224	665088	664126	963						
725	4225	666313	665183	1131	gp AF052652_1	Corynebacterium glutamicum metA	99.5	99.5	379	homoserine O-acetyltransferase
726	4226	667770	666460	1311	prf 2317335A	Leptospira meyeri metY	49.7	76.2	429	O-acetylhomoserine sulfhydrylase
727	4227	668264	670465	2202	sp CSTA_ECOLI	Escherichia coli K12 cstA	53.9	78.4	690	carbon starvation protein
728	4228	670053	669445	609						
729	4229	670472	670672	201	sp YJIX_ECOLI	Escherichia coli K12 yjiX	40.0	66.0	50	hypothetical protein
730	4230	671653	671045	609						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
731	4231	671700	672653	954	pir C70539	Mycobacterium tuberculosis H37Rv Rv1130	71.0	86.4	317	hypothetical protein
732	4232	672665	673576	912	prf 1902224A	Streptomyces hygroscopicus	41.6	76.2	281	carboxy phosphoenolpyruvate mutase
733	4233	673608	674756	1149	sp CISY_MYCSM	Mycobacterium smegmatis ATCC 607 gltA	56.1	81.3	380	citrate synthase
734	4234	673639	672710	930						
735	4235	674999	674799	201	sp YNEC_ECOLI	Escherichia coli K12 yneC	34.0	62.3	53	hypothetical protein
736	4236	675175	675846	672						
737	4237	676122	675082	1041	sp MDH_METFE	Methanothermus fervidus V24S mdh	37.6	67.5	338	L-malate dehydrogenase
738	4238	676937	676218	720	prf 2514353L	Bacillus stearothermophilus T-6 uxuR	26.1	62.8	226	regulatory protein
739	4239	677748	677047	702						
740	4240	681027	680131	897	sp VUB_VIBCH	Vibrio cholerae OGAWA 395 viuB	25.4	54.2	284	vibriobactin utilization protein
741	4241	681846	681040	807	gp AF176902_3	Corynebacterium diphtheriae irp1D	55.4	85.1	269	ABC transporter ATP-binding protein
742	4242	682904	681846	1059	gp AF176902_2	Corynebacterium diphtheriae irp1C	56.3	86.4	339	ABC transporter
743	4243	683866	682871	996	gp AF176902_1	Corynebacterium diphtheriae irp1B	63.0	88.2	330	ABC transporter
744	4244	684925	683876	1050	gp CDU02617_1	Corynebacterium diphtheriae irp1	53.1	82.3	356	iron-regulated lipoprotein precursor
745	4245	685109	686380	1272	prf 2202262A	Streptomyces venezuelae cmlv	32.2	69.6	395	chloramphenicol resistance protein
746	4246	686435	687346	912	prf 2222220B	Pseudomonas aeruginosa crc	30.4	58.1	303	catabolite repression control protein
747	4247	687351	688007	657	sp YIC3_HAEIN	Haemophilus influenzae Rd HI1240	56.2	85.8	219	hypothetical protein
748	4248	688141	688335	195						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
749	4249	689890	688916	975						
750	4250	690696	689917	780	gp AF109162_3	Corynebacterium diphtheriae hmuV	45.1	73.8	244	ferrichrome ABC transporter
751	4251	691722	690706	1017	pir S54438	Yersinia enterocolitica hemU	38.7	69.1	346	hemin permease
752	4252	691882	692916	1035	sp SYW_ECOLI	Escherichia coli K12 trpS	54.4	79.8	331	tryptophanyl-tRNA synthetase
753	4253	693028	694110	1083	sp YHJD_ECOLI	Escherichia coli K12 yhjD	37.1	72.3	278	hypothetical protein
754	4254	694172	695074	903						
755	4255	696213	695077	1137	sp DACD_SALTY	Salmonella typhimurium LT2 dacD	30.9	57.5	301	penicillin-binding protein 6B precursor
756	4256	697995	696769	1227	pir F70842	Mycobacterium tuberculosis H37Rv Rv3311	34.1	70.7	417	hypothetical protein
757	4257	698922	698065	858	gp SC6G10_8	Streptomyces coelicolor A3(2) SC6G10.08c	29.4	52.6	323	hypothetical protein
758	4258	699072	699266	195						
759	4259	699272	698922	351						
760	4260	699281	699913	633	sp UPP_LACLA	Lactococcus lactis upp	46.4	72.3	209	uracil phosphoribosyltransferase
761	4261	699998	700381	384	gp SC1A2_11	Streptomyces coelicolor A3(2) SC1A2.11	41.6	66.2	77	bacterial regulatory protein, lacI family
762	4262	702081	703262	1182	pir H70841	Mycobacterium tuberculosis H37Rv Rv3305c amiA	51.4	80.5	385	N-acyl-L-amino acid amidohydrolase or peptidase
763	4263	702108	700384	1725	sp MANB_MYCPI	Mycoplasma pirum BER manB	22.1	53.8	561	phosphomannomutase
764	4264	703405	704811	1407	sp DLDH_HALVO	Halobacterium volcanii ATCC 29605 lpd	31.6	65.0	468	dihydrolipoamide dehydrogenase
765	4265	705211	708630	3420	prf 2415454A	Corynebacterium glutamicum strain21253 pyc	100.0	100.0	1140	pyruvate carboxylase
766	4266	708839	709708	870	sp YD24_MYCTU	Mycobacterium tuberculosis H37Rv Rv1324	26.2	60.1	263	hypothetical protein
767	4267	709733	710278	486	gp SCF11_30	Streptomyces coelicolor A3(2) SCF11.30	30.7	66.9	127	hypothetical protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
768	4268	714605	715520	1086	pir B69760	Bacillus subtilis 168 yciC	44.6	69.0	381	hypothetical protein
769	4269	715524	716647	924	sp TRXB_BACSU	Bacillus subtilis IS59 trxB	24.6	59.3	305	thioredoxin reductase
770	4270	712738	714231	1494	sp PRPD_SALTY	Salmonella typhimurium LT2 prpD	24.0	49.5	521	PrpD protein for propionate catabolism
771	4271	714258	715145	888	prf 1900224A	Streptomyces hygroscopicus	42.5	74.5	278	carboxy phosphoenolpyruvate mutase
772	4272	714757	714380	378	PIR E72779	Aeropyrum pernix K1 APE0223	39.0	47.0	96	hypothetical protein
773	4273	715102	716283	1182	sp CISY_MYCSM	Mycobacterium smegmatis ATCC 607 gltA	54.6	78.9	383	citrate synthase
774	4274	716660	716286	375						
775	4275	718009	716687	1323	pir B70539	Mycobacterium tuberculosis H37Rv Rv1129c	40.8	72.6	456	hypothetical protein
776	4276	718105	718350	246						
777	4277	718658	720016	1359						
778	4278	721449	720547	903	sp THTR_CORGL	Corynebacterium glutamicum ATCC 13032 thtR	100.0	100.0	225	thiosulfate sulfurtransferase
779	4279	721777	722841	1065	gp CJ11168X1_62	Campylobacter jejuni CJ0069	61.1	79.8	352	hypothetical protein
780	4280	723338	722925	414	gp MLCB4_16	Mycobacterium leprae MLCB4.27c	51.1	76.7	133	hypothetical protein
781	4281	723412	725559	2148	pir G70539	Mycobacterium tuberculosis H37Rv Rv1565c	35.1	63.4	718	hypothetical membrane protein
782	4282	726462	725872	591	sp YCEF_ECOLI	Escherichia coli K12 yceF	31.8	66.2	192	hypothetical protein
783	4283	726715	726470	246	prf 2323363CF	Mycobacterium leprae B1308-C3-211	33.3	69.8	63	hypothetical protein
784	4284	728352	726742	1611	gp AB018531_2	Corynebacterium glutamicum AJ11060 dtsR2	99.8	100.0	537	detergent sensitivity rescuer or carboxyl transferase
785	4285	730324	728696	1629	pir JC4991	Corynebacterium glutamicum AJ11060 dtsR1	99.6	100.0	543	detergent sensitivity rescuer or carboxyl transferase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
786	4286	730436	731299	864	sp BIRA_ECOLI	Escherichia coli K12 birA	28.7	61.8	293	bifunctional protein (biotin synthesis repressor and biotin acetyl-CoA carboxylase ligase)
787	4287	731312	731797	486	pir G70979	Mycobacterium tuberculosis H37Rv Rv3278c	23.0	58.8	165	hypothetical membrane protein
788	4288	731857	733017	1161	sp PURK_CORAM	Corynebacterium ammoniagenes ATCC 6872 purK	69.0	83.8	394	5'-phosphoribosyl-5-amino-4-imidasol carboxylase
789	4289	733072	734943	1872	sp KUP_ECOLI	Escherichia coli K12 kup	41.1	73.6	628	K+-uptake protein
790	4290	733797	733183	615						
791	4291	734984	735340	357						
792	4292	735402	735896	495	sp PUR6_CORAM	Corynebacterium ammoniagenes ATCC 6872 purE	85.7	93.2	147	5'-phosphoribosyl-5-amino-4-imidasol carboxylase
793	4293	735899	736351	453	gp APU33059_5	Actinosynnema pretiosum	36.2	60.5	152	hypothetical protein
794	4294	736413	737204	792	gp SCF43A_36	Streptomyces coelicolor A3(2) SCF43A.36	42.8	70.6	255	hypothetical protein
795	4295	738529	737216	1314	sp NTAA_CHEHE	Chelatobacter heintzii ATCC 29600 ntaA	43.2	73.0	426	nitrilotriacetate monooxygenase
796	4296	740172	738673	1500	pir A69426	Archaeoglobus fulgidus	23.4	52.5	303	transposase (ISA0963-5)
797	4297	741016	740228	789	sp DHG2_BACME	Bacillus megaterium IAM 1030 gdhII	31.3	64.8	256	glucose 1-dehydrogenase
798	4298	741397	741765	369	pir A72258	Thermotoga maritima MSB8 TM1408	29.2	68.8	96	hypothetical membrane protein
799	4299	741854	742195	342						
800	4300	742384	741818	567	sp YWJB_BACSU	Bacillus subtilis 168 ywjB	28.6	66.3	175	hypothetical protein
801	4301	742409	742828	420	gp SCJ9A_21	Streptomyces coelicolor A3(2) SCJ9A.21	35.9	76.8	142	hypothetical protein
802	4302	743052	742831	222						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
803	4303	743900	743067	834	prf 2406355C	Thermococcus litoralis malG	42.4	75.3	271	trehalose/maltose-binding protein
804	4304	744931	743900	1032	prf 2406355B	Thermococcus litoralis malF	37.3	70.3	306	trehalose/maltose-binding protein
805	4305	745513	745046	468						
806	4306	746893	745622	1272	prf 2406355A	Thermococcus litoralis malE	30.9	62.4	417	trehalose/maltose-binding protein
807	4307	748020	748442	423						
808	4308	748026	747031	996	prf 2308336A	Streptomyces reticuli msiK	57.2	73.9	332	ABC transporter ATP-binding protein (ABC-type sugar transport protein) or cellobiose/maltose transport protein
809	4309	748446	748814	369						
810	4310	753685	748886	4800	pir B75633	Deinococcus radiodurans R1 DR0135	25.1	49.9	1783	RNA helicase
811	4311	757063	757434	372						
812	4312	757395	753697	3699						
813	4313	759262	757630	633	pir E70978	Mycobacterium tuberculosis H37Rv Rv3268	31.7	59.2	240	hypothetical protein
814	4314	760796	758364	2433	pir C71929	Helicobacter pylori J99 jhp0462	30.0	62.5	720	hypothetical protein
815	4315	762468	760906	1563	sp UVRD_ECOLI	Escherichia coli K12 uvrD	20.7	41.1	701	DNA helicase II
816	4316	762497	762853	357						
817	4317	762730	763122	393						
818	4318	762977	762582	396						
819	4319	768191	767367	825						
820	4320	769443	763237	6207	pir T36671	Streptomyces coelicolor SCH5.13	22.4	45.8	2033	RNA helicase
821	4321	774142	769547	4596	pir T08313	Halobacterium sp. NRC-1 plasmid pNRC100 H1130	24.4	53.2	698	hypothetical protein
822	4322	777035	774150	2886	sp HEPA_ECOLI	Escherichia coli K12 hepA	23.1	48.6	873	RNA polymerase associated protein (ATP-dependent helicase)

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initia' (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
823	4323	778711	777158	1554	pir D70978	Mycobacterium tuberculosis H37Rv Rv3267	45 5	71 4	527	hypothetical protein
824	4324	779014	779910	897	gp AF187550_1	Mycobacterium smegmatis mc2155 wbbL	56 4	77 9	289	dTDP-Rha a-D-GlcNAc-diphosphoryl polyprenol, a 3-L rhamnosyl transferase
825	4325	780128	781171	1044	sp MPG1_YEAST	Saccharomyces cerevisiae YDL055C MPG1	29 8	66 9	353	mannose-1-phosphate guanylyltransferase
826	4326	781468	781875	408	gp AF164439_1	Mycobacterium smegmatis whmD	73 4	81 9	94	regulatory protein
827	4327	782617	782162	456	pir B70847	Mycobacterium tuberculosis H37Rv Rv3259	48 9	74 8	139	hypothetical protein
828	4328	782712	783101	390	gp SCE34_11	Streptomyces coelicolor A3(2) SCE34.11c	51 5	71 3	136	hypothetical protein
829	4329	783184	784557	1374	sp MANB_SALMO	Salmonella montevideo M40 manB	38 0	66 3	460	phosphomannomutase
830	4330	784635	785639	1005	pir B70594	Mycobacterium tuberculosis H37Rv Rv3256c	31 2	56 3	327	hypothetical protein
831	4331	785643	786824	1182	sp MANA_ECOLI	Escherichia coli K12 manA	36 9	66 2	420	mannose-6-phosphate isomerase
832	4332	785896	787045	150						
833	4333	787624	787983	360						
834	4334	787733	787170	564	prf 1804279K	Enterococcus faecalis plasmid pCF10 prgC	35 6	57 8	180	pheromone-responsive protein
835	4335	788196	788546	351						
836	4336	788672	790093	1422	sp SAHH_TRIVA	Trichomonas vaginalis WAA38	59 0	83 0	476	S-adenosyl-L-homocysteine hydrolase
837	4337	789426	788719	708						
838	4338	789721	789002	720						
839	4339	790096	790704	609	sp KTHY_ARCFU	Archaeoglobus fulgidus VC-16 AF0061	25 8	56 0	209	thymidylate kinase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
840	4340	790732	791409	678	prf 2214304A	Mycobacterium tuberculosis H37Rv Rv3246c mtrA	73.7	90.6	224	two-component system response regulator
841	4341	791421	790738	684						
842	4342	791512	793008	1497	prf 2214304B	Mycobacterium tuberculosis H37Rv Rv3245c mtrB	53.1	78.9	484	two-component system sensor histidine kinase
843	4343	793008	794711	1704	pir F70592	Mycobacterium tuberculosis H37Rv Rv3244c lpqB	29.6	65.6	595	lipoprotein
844	4344	794714	795301	588	pir D70592	Mycobacterium tuberculosis H37Rv Rv3242c	38.0	72.8	213	hypothetical protein
845	4345	795447	795292	156						
846	4346	795448	796110	663	sp RR30_SPIOL	Spinacia oleracea CV rps22	34.5	61.6	203	30S ribosomal protein or chloroplast precursor
847	4347	796250	798784	2535	gsp R74093	Brevibacterium flavum (Corynebacterium glutamicum) MJ-233 secA	99.1	99.6	845	preprotein translocase SecA subunit
848	4348	799020	799691	672						
849	4349	799697	800200	504	pir A70591	Mycobacterium tuberculosis H37Rv Rv3231c	47.1	78.8	170	hypothetical protein
850	4350	801194	800208	987	pir F70590	Mycobacterium tuberculosis H37Rv Rv3228	64.6	82.9	322	hypothetical protein
851	4351	802602	801190	1413	gp AF114233_1	Corynebacterium glutamicum ASO19 aroA	99.0	99.0	461	5-enolpyruvylshikimate 3-phosphate synthase
852	4352	802649	802128	480	pir D70590	Mycobacterium tuberculosis H37Rv Rv3226c	38.3	63.9	180	hypothetical protein
853	4353	802687	802565	123	GP AF114233_1	Corynebacterium glutamicum	100.0	100.0	23	5-enolpyruvylshikimate 3-phosphate synthase
854	4354	804240	803131	1110	pir G70506	Mycobacterium tuberculosis H37Rv Rv0336	21.6	42.4	380	hypothetical protein
855	4355	804408	805025	618	prf 2515333D	Mycobacterium tuberculosis sigH	61.2	87.2	188	RNA polymerase sigma factor

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
856	4356	805792	805535	258	pir D70596	Mycobacterium tuberculosis H37Rv Rv3219 whiB1	78 6	96 4	84	regulatory protein
857	4357	806318	806737	420	pir B70596	Mycobacterium tuberculosis H37Rv Rv3217c	33 3	65 1	129	hypothetical protein
858	4358	807939	806740	1200	pir E70595	Mycobacterium tuberculosis H37Rv Rv3212	29 6	62 2	415	hypothetical protein
859	4359	809217	807946	1272	sp DEAD_KLEPN	Klebsiella pneumoniae CG43 deaD	37 3	64 0	458	DEAD box ATP-dependent RNA helicase
860	4360	809286	809510	225						
861	4361	809549	810394	846	pir H70594	Mycobacterium tuberculosis H37Rv Rv3207c	46 4	69 8	291	hypothetical protein
862	4362	810405	811163	759	pir F70594	Mycobacterium tuberculosis H37Rv Rv3205c	37 0	65 9	249	hypothetical protein
863	4363	811170	814217	3048	pir G70951	Mycobacterium tuberculosis H37Rv Rv3201c	23 9	48 9	1155	ATP-dependent DNA helicase
864	4364	812165	811386	780						
865	4365	814204	817422	3219	pir G70951	Mycobacterium tuberculosis H37Rv Rv3201c	41 4	65 7	1126	ATP-dependent DNA helicase
866	4366	815541	814210	1332						
867	4367	817519	818523	1005	sp Y13B_METJA	Methanococcus jannaschii JAL-1 MJ0138 1	26 2	64 2	302	potassium channel
868	4368	818523	819236	714	pir E70951	Mycobacterium tuberculosis H37Rv Rv3199c	30 4	58 3	230	hypothetical protein
869	4369	819254	821287	2034	sp UVRD_ECOLI	Escherichia coli K12 uvrD	32 6	58 8	660	DNA helicase II
870	4370	822079	822669	591						
871	4371	822105	821290	816	pir B70951	Mycobacterium tuberculosis H37Rv Rv3196	26 8	49 3	280	hypothetical protein
872	4372	822789	823391	603						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
873	4373	824125	822680	1446	pir A70951	Mycobacterium tuberculosis H37Rv Rv3195	42 8	76 4	474	hypothetical protein
874	4374	824180	825239	1050	pir H70950	Mycobacterium tuberculosis H37Rv Rv3194	43 4	74 9	350	hypothetical protein
875	4375	825916	825242	675						
876	4376	826517	825996	522						
877	4377	825616	829570	2955	pir G70950	Mycobacterium tuberculosis H37Rv Rv3193c	47.2	73 5	1023	hypothetical protein
878	4378	830985	829627	1359	gp AE001938_5	Deinococcus radiodurans DR0840	34 3	57.7	463	regulatory protein
879	4379	831021	831971	951	sp ER1_HEVBR	Hevea brasiliensis laticifer er1	67 4	89 0	301	ethylene-inducible protein
880	4380	831922	831578	345	PIR F72782	Aeropyrum pernix K1 APE0247	49 0	53 0	81	hypothetical protein
881	4381	831971	832570	600	sp YAAE_BACSU	Bacillus subtilis 168 yaaE	40.8	73 6	201	hypothetical protein
882	4382	833157	832795	363						
883	4383	833572	834633	1062	pir TRYXB4	Lysobacter enzymogenes ATCC 29487	26.7	44 4	408	alpha-lytic proteinase precursor
884	4384	834888	835388	501						
885	4385	835253	835837	585	pir S03722	Neurospora intermedia I aBelle-1b mitochondrion plasmid	25 0	51 4	208	DNA-directed DNA polymerase
886	4386	837312	838892	1581	sp CSP1_CORGL	Corynebacterium glutamicum (Brevibacterium flavum) ATCC 17965 csp1	27.0	51 5	363	major secreted protein PS1 protein precursor
887	4387	838925	839353	429						
888	4388	839630	840139	510						
889	4389	840431	840210	222						
890	4390	840745	840437	309						
891	4391	842296	841517	780	pir S20727\3H	Streptomyces alboniger pur3	51 8	74 9	255	monophosphatase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
892	4392	843124	842306	819	gp:U70376_9	Streptomyces flavopersicus spcA	33.7	59.3	243	myo-inositol monophosphatase
893	4393	843257	844360	1104	sp:RF2_STRCO	Streptomyces coelicolor A3(2) prfB	68.0	88.6	359	peptide chain release factor 2
894	4394	844495	845181	687	pir:E70919	Mycobacterium tuberculosis H37Rv Rv3102c ftsE	70.4	91.2	226	cell division ATP-binding protein
895	4395	845105	844842	264	PIR:C72510	Aeropyrum pernix K1 APE2061	43.0	54.0	72	hypothetical protein
896	4396	845198	846097	900	pir:D70919	Mycobacterium tuberculosis H37Rv Rv3101c ftsX	40.5	74.8	301	cell division protein
897	4397	846137	846628	492	sp:SMPB_ECOLI	Escherichia coli K12 smpB	43.5	75.9	145	small protein B (SSRA-binding protein)
898	4398	846632	846982	351	sp:YEAO_ECOLI	Escherichia coli K12 yeaO	44.0	73.3	116	hypothetical protein
899	4399	846805	846269	537						
900	4400	847727	848026	300						
901	4401	848122	847718	405						
902	4402	849323	848499	825	sp:VIUB_VIBCH	Vibrio cholerae OGAWA 395 viuB	26.8	52.9	272	vibriobactin utilization protein
903	4403	850243	849326	918	prf:2510361A	Staphylococcus aureus sirA	29.5	58.3	319	Fe-regulated protein
904	4404	850099	850412	588	gp:MLCB1243_5	Mycobacterium leprae MLCB1243.07	36.1	71.2	191	hypothetical membrane protein
905	4405	851351	852364	1014	sp:FATB_VIBAN	Vibrio anguillarum 775 fatB	27.7	61.5	325	ferric anguibactin-binding protein precursor
906	4406	852618	853616	999	pir:B69763	Bacillus subtilis 168 yclN	39.3	80.8	313	ferrichrome ABC transporter (permease)
907	4407	853783	854724	942	pir:C69763	Bacillus subtilis 168 yclO	35.6	76.0	312	ferrichrome ABC transporter (permease)
908	4408	854724	855476	753	pir:D69763	Bacillus subtilis 168 yclP	48.4	82.0	250	ferrichrome ABC transporter (ATP-binding protein)

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initia (nt)	Termina (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
909	4409	860224	860078	147	PIR F81737	Chlamydia muridarum Nigg TC0129	66.0	72.0	48	hypothetical protein
910	4410	860745	860473	273	GSP Y35814	Chlamydia pneumoniae	61.0	66.0	84	hypothetical protein
911	4411	861544	862752	1209	pir S66270	Rattus norvegicus (Rat)	33.5	64.9	442	kynurenine aminotransferase/glutamine transaminase K
912	4412	863391	862753	639						
913	4413	865066	863396	1671	sp RA25_YEAST	Saccharomyces cerevisiae S288C YIL143C RAD25	30.7	62.3	613	DNA repair helicase
914	4414	867317	865119	2199	pir F70815	Mycobacterium tuberculosis H37Rv Rv0862c	36.1	65.2	764	hypothetical protein
915	4415	867353	867571	219	pir G70815	Mycobacterium tuberculosis H37Rv Rv0863	44.0	62.0	57	hypothetical protein
916	4416	867788	868630	843						
917	4417	868399	867803	597	prf 2420502A	Micrococcus luteus rpf	39.4	64.7	198	resuscitation-promoting factor
918	4418	868938	869318	381	prf 2320271A	Lactococcus lactis cspB	42.6	75.4	61	cold shock protein
919	4419	869903	869379	525	gp MLCB57_11	Mycobacterium leprae MLCB57.27c	28.3	58.5	159	hypothetical protein
920	4420	870691	869918	774	gp AE001874_1	Deinococcus radiodurans DR0112	41.8	67.8	273	glutamine cyclotransferase
921	4421	871419	870721	699						
922	4422	871523	871660	138						
923	4423	871738	873210	1473	gp SC6C5_9	Streptomyces coelicolor A3(2) SC6C5.09	43.6	79.3	477	permease
924	4424	872927	872016	912						
925	4425	873213	874040	828	sp TSNR_STRAZ	Streptomyces azureus tsnR	27.9	51.7	319	rRNA(adenosine-2'-O-)-methyltransferase
926	4426	874944	874069	876						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
927	4427	875883	874951	933	sp:YZ11_MYCTU	Mycobacterium tuberculosis H37Rv Rv0883c	32.6	55.1	316	hypothetical protein
928	4428	877112	875985	1128	pir S71439	Bacillus circulans ATCC 21783	21.9	52.9	374	phosphoserine transaminase
929	4429	881114	879642	1473	sp:ACCD_ECOLI	Escherichia coli K12 accD	36.0	69.5	236	acetyl-coenzyme A carboxylase carboxy transferase subunit beta
930	4430	881647	881985	339	gp:SCI8_8	Streptomyces coelicolor A3(2) SCI8.08c	51.5	80.6	103	hypothetical protein
931	4431	881995	883647	1653	pir JC2382	Pseudomonas fluorescens	26.4	58.1	549	sodium/proline symporter
932	4432	883726	884541	816						
933	4433	885388	884549	840	pir A70657	Mycobacterium tuberculosis H37Rv Rv2525c	49.0	77.4	243	hypothetical protein
934	4434	885672	894578	8907	pir S55505	Corynebacterium ammoniagenes fas	63.1	83.4	3026	fatty acid synthase
935	4435	894703	895191	489						
936	4436	895408	895593	186						
937	4437	896642	895596	1047	prf:2317335B	Leptospira meyeri metX	29.0	59.7	335	homoserine O-acetyltransferase
938	4438	897144	896719	426						
939	4439	897423	897689	267						
940	4440	897963	897727	237	gp:AE002044_8	Deinococcus radiodurans DR2085	43.6	72.5	62	glutaredoxin
941	4441	898434	897979	456	prf:2408256A	Mycobacterium avium folA	38.0	62.0	171	dihydrofolate reductase
942	4442	899231	898434	798	sp:TYSY_ECOLI	Escherichia coli K12 thyA	64.8	88.9	261	thymidylate synthase
943	4443	900008	899253	756	sp:CYSQ_ECOLI	Escherichia coli K12 cysQ	32.2	56.4	202	ammonium transporter
944	4444	900043	904602	4560	gp:SC7C7_16	Streptomyces coelicolor A3(2) SC7C7.16c	47.4	68.1	1715	ATP dependent DNA helicase
945	4445	904615	905382	768	sp:FPG_SYNEN	Synechococcus elongatus naegeli mutM	29.2	51.0	298	formamidopyrimidine-DNA glycosidase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
946	4446	905389	905796	408	pir F70816	Mycobacterium tuberculosis H37Rv Rv0870c	55.5	86.7	128	hypothetical protein
947	4447	906391	905792	600	sp APL_LACLA	Lactococcus lactis MG1363 apl	38.8	71.9	196	alkaline phosphatase
948	4448	907731	906559	1173	pir T36776	Streptomyces coelicolor A3(2) SCI28.06c	33.8	67.0	403	integral membrane transporter
949	4449	908612	909328	717						
950	4450	909378	907759	1620	pir NUEC	Escherichia coli JM101 pgi	52.4	77.0	557	glucose-6-phosphate isomease
951	4451	910696	909521	1176	pir G70506	Mycobacterium tuberculosis H37Rv Rv0336	24.6	52.3	195	hypothetical protein
952	4452	910843	911223	381						
953	4453	911163	910855	309	sp YT26_MYCTU	Mycobacterium tuberculosis H37Rv Rv0948c	59.0	85.9	78	hypothetical protein
954	4454	911226	913514	2289	sp PCRA_BACST	Bacillus stearothermophilus NCA 1503 pcrA	46.1	73.1	763	ATP-dependent helicase
955	4455	915699	913477	2223	gp SCE25_30	Streptomyces coelicolor A3(2) SCE25.30	21.8	48.6	885	ABC transporter
956	4456	916364	915699	666	prf 2420410P	Bacillus subtilis 168 yvrO	43.8	71.4	217	ABC transporter
957	4457	916874	916368	507						
958	4458	917680	916970	711	pir D70716	Mycobacterium tuberculosis H37Rv Rv0950c	43.6	73.3	236	peptidase
959	4459	917928	919352	1425	sp YT19_MYCTU	Mycobacterium tuberculosis H37Rv Rv0955	31.1	60.8	434	hypothetical protein
960	4460	918054	917827	228						
961	4461	919330	919956	627	gp AB003159_2	Corynebacterium ammoniagenes purN	64.6	86.2	189	5'-phosphoribosylglycinamide formyltransferase
962	4462	919967	921526	1560	gp AB003159_3	Corynebacterium ammoniagenes purH	74.5	87.8	525	5'-phosphoribosyl-5-aminoimidazole-4-carboxamide formyltransferase
963	4463	921594	922412	819	gp CGL133719_3	Corynebacterium glutamicum ATCC 13032 citE	100.0	100.0	217	citrate lyase (subunit)

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
964	4464	923061	922396	666	gp:CGL133719_2	Corynebacterium glutamicum ATCC 13032 amtR	100.0	100.0	222	repressor of the high-affinity (methyl) ammonium uptake system
965	4465	923464	923138	327	gp:CGL133719_1	Corynebacterium glutamicum ATCC 13032 yjcC	100.0	100.0	109	hypothetical protein
966	4466	923661	923981	321						
967	4467	924407	924159	249	sp:RR18_CYAPA	Cyanophora paradoxa rps18	52.2	76.1	67	30S ribosomal protein S18
968	4468	924727	924425	303	sp:RS14_ECOLI	Escherichia coli K12 rpsN	54.0	80.0	100	30S ribosomal protein S14
969	4469	924895	924734	162	sp:RL33_ECOLI	Escherichia coli K12 rpmG	55.1	83.7	49	50S ribosomal protein L33
970	4470	925134	924901	234	pir:R5ECRB	Escherichia coli K12 rpmB	52.0	81.8	77	50S ribosomal protein L28
971	4471	926935	925326	1611	pir:B70033	Bacillus subtilis 168 yvdB	34.4	71.1	529	transporter (sulfate transporter)
972	4472	927242	926931	312	pir:2420312A	Staphylococcus aureus zntR	37.5	77.5	80	Zn/Co transport repressor
973	4473	927474	927737	264	sp:RL31_HAEDU	Haemophilus ducreyi rpmE	37.2	65.4	78	50S ribosomal protein L31
974	4474	927752	927922	171	gp:SCF51A_14	Streptomyces coelicolor A3(2) SCF51A.14	60.0	78.2	55	50S ribosomal protein L32
975	4475	927785	927339	447						
976	4476	928117	928812	696	sp:COPR_PSESM	Pseudomonas syringae copR	48.0	73.6	227	copper-inducible two-component regulator
977	4477	928884	930248	1365	sp:BAES_ECOLI	Escherichia coli K12 baeS	24.4	60.1	484	two-component system sensor
978	4478	930410	931648	1239	pir:S45229	Escherichia coli K12 htrA	33.3	59.9	406	proteinase DO precursor
979	4479	931706	932290	585	sp:CNX1_ARATH	Arabidopsis thaliana CV cnx1	27.7	54.3	188	molybdopterin biosynthesis cnx1 protein (molybdenum cofactor biosynthesis enzyme cnx1)
980	4480	932290	932487	198						
981	4481	932974	932570	405	sp:MSCL_MYCTU	Mycobacterium tuberculosis H37Rv Rv0985c mscL	50.4	77.1	131	large-conductance mechanosensitive channel
982	4482	933710	933060	651	pir:A70601	Mycobacterium tuberculosis H37Rv Rv0990	28.6	60.0	210	hypothetical protein
983	4483	934302	933733	570	pir:JC4389	Homo sapiens MTHFS	25.1	59.7	191	5-formyltetrahydrofolate cyclo-ligase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
984	4484	934423	935319	897	pir JC4985	Xanthomonas campestris	42.2	68.9	296	UTP--glucose-1-phosphate uridyly transferase
985	4485	935351	936607	1257	prf 2403296B	Arthrobacter nicotinovorans moeA	31.8	62.6	390	molybdopterin biosynthesis protein
986	4486	936615	937274	660	sp RIMJ_ECOLI	Escherichia coli K12 rimJ	29.0	54.9	193	ribosomal-protein-alanine N-acetyltransferase
987	4487	937382	938401	1020	pir G70601	Mycobacterium tuberculosis H37Rv Rv0996	30.3	54.8	367	hypothetical membrane protein
988	4488	938427	939625	1200	sp CYNX_ECOLI	Escherichia coli K12 cynX	26.6	62.4	380	cyanate transport protein
989	4489	939217	937799	1419						
990	4490	939686	940090	405	sp YG02_HAEIN	Haemophilus influenzae Rd HI1602	32.1	60.6	137	hypothetical membrane protein
991	4491	940041	940754	714	sp Y05C_MYCTU	Mycobacterium tuberculosis H37Rv Rv0093c	25.3	59.6	225	hypothetical membrane protein
992	4492	940759	941925	1167	sp CDAS_BACSH	Bacillus sphaericus E-244 CDase	26.8	53.6	444	cyclomaltodextrinase
993	4493	943940	942381	1560	pir E70602	Mycobacterium tuberculosis H37Rv	43.0	75.2	488	hypothetical membrane protein
994	4494	944009	944833	825	sp Y19J_MYCTU	Mycobacterium tuberculosis H37Rv Rv1003	54.0	78.3	272	hypothetical protein
995	4495	946840	948669	1830	sp SYM_METTH	Methanobacterium thermoautotrophicum Delta H MTH587 metG	33.8	66.7	615	methionyl-tRNA synthetase
996	4496	948791	950839	2049	prf 1306383A	Escherichia coli recQ	26.2	49.0	741	ATP-dependent DNA helicase
997	4497	951460	950828	633	pir B69206	Methanobacterium thermoautotrophicum Delta H MTH796	27.6	53.3	210	hypothetical protein
998	4498	952991	951834	1158	sp YXAG_BACSU	Bacillus subtilis 168 yxaG	30.0	59.0	363	hypothetical protein
999	4499	953573	953043	531						
1000	4500	953973	954266	294	gp AF029727_1	Enterococcus faecium	33.0	59.6	94	transposase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (aa)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (aa)	Function
1001	4501	954277	954753	477	pir TQEC13	Escherichia coli K12	41.7	67.6	139	transposase
1002	4502	954941	955354	414	gp AF052055_1	Brevibacterium linens tnpA	73.2	88.4	112	transposase subunit
1003	4503	955911	956774	864						
1004	4504	957398	955686	1713	prf 2014253AF	Escherichia coli dld	46.4	75.6	565	D-lactate dehydrogenase
1005	4505	958683	957844	840	sp MTK1_KLEPN	Klebsiella pneumoniae OK8 kpnIM	30.8	62.8	231	site-specific DNA-methyltransferase
1006	4506	959403	959185	219						
1007	4507	960081	960374	294	gp AF329727_1	Enterococcus faecium	33.0	59.6	94	transposase
1008	4508	960385	960861	477	pir TQEC13	Escherichia coli K12	41.7	67.6	139	transposase
1009	4509	961297	961653	357	sp YJ94_MYCTU	Mycobacterium tuberculoss H37Rv Rv1994c	62.6	84.6	91	transcriptional regulator
1010	4510	961629	962249	621	prf 2514367A	Staphylococcus aureus cadD	31.7	66.8	205	cadmium resistance protein
1011	4511	961662	961321	342						
1012	4512	962809	963639	831	pir C70603	Mycobacterium tuberculosis H37Rv Rv1008	46.4	70.7	263	hypothetical protein
1013	4513	963864	964934	1071	pir D70603	Mycobacterium tuberculosis H37Rv Rv1009 rpf	34.8	63.5	362	hypothetical protein
1014	4514	964974	965852	879	sp KSGA_ECOLI	Escherichia coli K12 ksgA	34.3	65.3	265	dimethyladenosine transferase
1015	4515	965852	966784	933	pir F70603	Mycobacterium tuberculosis H37Rv Rv1011	42.5	67.0	315	isopentenyl monophosphate kinase
1016	4516	966591	965950	642						
1017	4517	966828	968660	1833	pir S47441	Saccharopolyspora erythraea ertX	65.5	85.8	478	ABC transporter
1018	4518	968667	969458	792	sp PDXK_ECOLI	Escherichia coli K12 pdxK	40.1	67.4	242	pyridoxine kinase
1019	4519	969940	969461	480	sp YA05_MYCTU	Mycobacterium tuberculosis H37Rv Rv2874	27.0	58.5	159	hypothetical protein
1020	4520	970029	970349	321	gp SCF1_2	Streptomyces coelicolor A3(2) SCF1.02	45.4	78.7	108	hypothetical protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1021	4521	970418	970739	321	gp SCF1_2	Streptomyces coelicolor A3(2) SCF1.02	35.5	69.2	107	hypothetical protein
1022	4522	970864	971823	960	gp SCJ1_15	Streptomyces coelicolor A3(2) SCJ1.15	64.8	88.1	261	regulator
1023	4523	972035	972244	792	sp YXEH_BACSU	Bacillus subtilis 168 yxeH	27.2	59.1	276	hypothetical protein
1024	4524	973139	974155	1017	pir E70893	Mycobacterium tuberculosis H37Rv echA9	35.6	70.9	337	enoyl-CoA hydratase
1025	4525	973957	973304	654						
1026	4526	974186	974962	777						
1027	4527	976176	974965	1212						
1028	4528	976349	977734	1386	sp CSP1_CORGL	Corynebacterium glutamicum (Brevibacterium flavum) ATCC 17965 csp1	27.7	56.8	440	major secreted protein PS1 protein precursor
1029	4529	978378	977800	579	gp SCF56_6	Streptomyces coelicolor A3(2) SCF56.06	44.0	70.0	100	transcriptional regulator (tetR family)
1030	4530	980740	978368	2373	gp SCE87_17	Streptomyces coelicolor A3(2) SCE87.17c	42.6	70.0	802	membrane transport protein
1031	4531	980993	981490	498	sp MENG_HAEIN	Haemophilus influenzae Rd HI0508 menG	38.2	75.8	157	S-adenosylmethionine 2-demethylmenaquinone methyltransferase
1032	4532	981622	982287	666						
1033	4533	982674	982294	381	gp NMA6Z2491_214	Neisseria meningitidis NMA1953	29.8	63.6	121	hypothetical protein
1034	4534	983100	984650	1551	pir A70539	Mycobacterium tuberculosis H37Rv Rv1128c	24.9	48.3	482	hypothetical protein
1035	4535	984910	985845	936						
1036	4536	986510	984864	1647	pir B59505	Escherichia coli K12 prfC	39.2	68.0	546	peptide-chain-release factor 3
1037	4537	986739	988007	1269	prf 2406311A	Methylophilus methylotrophus fmdD	42.8	72.8	404	amide-urea transport protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1038	4538	988023	988904	882	prf 2406311B	Methylophilus methylotrophus fmdE	40 8	61 0	77	amide-urea transport protein
1039	4539	988904	989980	1077	prf 2406311C	Methylophilus methylotrophus fmdF	34 6	68 0	234	amide-urea transport protein
1040	4540	989980	990705	726	sp BRAF_PSEAE	Pseudomonas aeruginosa PAO braF	37 9	70 0	253	high-affinity branched-chain amino acid transport ATP-binding protein
1041	4541	990716	991414	699	sp BRAG_PSEAE	Pseudomonas aeruginosa PAO braG	35 2	69 1	236	high-affinity branched-chain amino acid transport ATP-binding protein
1042	4542	992028	991417	612	sp PTH_ECOLI	Escherichia coli K12 pth	39 0	70 6	187	peptidyl-tRNA hydrolase
1043	4543	992058	993080	1023	sp 2NPD_WILMR	Williopsis mrakii IFO 0895	25 2	54 0	361	2-nitropropane dioxygenase
1044	4544	993549	994613	1065	sp G3P_ZYMMO	Streptomyces roseofulvus gap	39 5	72 8	342	glyceraldehyde-3-phosphate dehydrogenase
1045	4545	994474	994106	369	GSP Y75094	Neisseria meningitidis	54 0	61 0	51	polypeptides predicted to be useful antigens for vaccines and diagnostics
1046	4546	995375	994845	531	sp PTH_ECOLI	Escherichia coli K12 pth	38 5	63 2	174	peptidyl-tRNA hydrolase
1047	4547	996126	995527	600	pir B70622	Mycobacterium tuberculosis H37Rv rplY	47 0	65 0	194	50S ribosomal protein L25
1048	4548	996402	996830	429	sp LGUL_SALTY	Salmonella typhimurium D21 gloA	28 7	54 6	143	lactoylglutathione lyase
1049	4549	997456	996833	624	prf 2516401BW	Bacillus cereus ATCC 10987 alkD	38 9	62 5	208	DNA alkylation repair enzyme
1050	4550	998440	997466	975	sp KPRS_BACCL	Bacillus subtilis prs	44 0	79 1	316	ribose-phosphate pyrophosphokinase
1051	4551	999909	998455	1455	pir S66080	Bacillus subtilis gcaD	42 0	71 9	452	UDP-N-acetylglucosamine pyrophosphorylase
1052	4552	1001242	1000016	1227						
1053	4553	1001332	1002864	1533	sp SUFI_ECOLI	Escherichia coli K12 sufI	30 8	61 7	506	sufI protein precursor
1054	4554	1003013	1003930	918	sp NODI_RHIS3	Rhizobium sp. N33 nodI	35 8	64 8	310	nodulation ATP-binding protein I

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
1055	4555	1003953	1004793	831	pir JN0850	Streptomyces lividans ORF2	30.2	63.2	272	hypothetical membrane protein
1056	4556	1004829	1006085	1257	sp UHPB_ECOLI	Escherichia coli K12 uhpB	24.6	48.4	459	two-component system sensor histidine kinase
1057	4557	1006089	1006697	609	prf 2107255A	Streptomyces peucetius dnrN	36.6	67.3	202	two component transcriptional regulator (luxR family)
1058	4558	1006937	1006734	204						
1059	4559	1006998	1008152	1155	gp SCF15_7	Streptomyces coelicolor A3(2) SCF15.07	31.5	64.5	349	hypothetical membrane protein
1060	4560	1008522	1010061	1440	pir S65587	Streptomyces glaucescens strV	28.6	57.0	535	ABC transporter
1061	4561	1008686	1008534	153						
1062	4562	1010057	1011790	1734	pir T14180	Mycobacterium smegmatis exiT	44.0	74.0	573	ABC transporter
1063	4563	1013761	1011797	1965	sp GGT_ECOLI	Escherichia coli K12 ggt	32.4	58.6	666	gamma-glutamyltranspeptidase precursor
1064	4564	1014016	1014264	249						
1065	4565	1014861	1014343	519						
1066	4566	1014925	1015116	192						
1067	4567	1015652	1016560	909						
1068	4568	1015692	1015450	243	GPU AF164956_23	Corynebacterium glutamicum TnpNC	64.0	72.0	37	transposase protein fragment
1069	4569	1015852	1015145	708	gp AF121000_8	Corynebacterium glutamicum 22243 R-plasmid pAG1 tnpB	99.6	100.0	236	transposase (IS1628 TnpB)
1070	4570	1016557	1017018	462						
1071	4571	1017870	1017274	597						
1072	4572	1018082	1018393	312						
1073	4573	1018416	1019066	651	sp TETC_ECOLI	Escherichia coli tetR	23.0	59.6	183	transcriptional regulator (TetR-family)
1074	4574	1019030	1022715	3627	sp MFD_ECOLI	Escherichia coli mfd	36.2	65.1	1217	transcription/repair-coupling protein
1075	4575	1020613	1019390	1224						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1076	4576	1021305	1021078	228	GSP:Y75301	Neisseria gonorrhoeae	48 0	69 0	76	Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics
1077	4577	1024666	1022699	1968	sp MDLB_ECOLI	Escherichia coli mdlB	31 3	62 7	632	multidrug resistance like ATP binding protein, ABC-type transport protein
1078	4578	1026396	1024666	1731	sp YC73_MYCTU	Mycobacterium tuberculosis H37Rv Rv1273c	50 2	81 9	574	ABC transporter
1079	4579	1028886	1026505	2382	sp YLI3_CORGL	Corynebacterium glutamicum ATCC 13032 orf3	100 0	100 0	368	hypothetical membrane protein
1080	4580	1031885	1032181	297						
1081	4581	1032196	1032780	585	sp YABN_BACSU	Bacillus subtilis yabN	33 4	57 4	183	hypothetical protein
1082	4582	1033185	1032760	426						
1083	4583	1033646	1033269	378						
1084	4584	1033954	1034739	786	pir A70623	Mycobacterium tuberculosis H37Rv Rv1022 lpqU	46 5	68 9	241	lpqU protein
1085	4585	1034949	1036223	1275	sp ENO_BACSU	Bacillus subtilis eno	64 5	86 0	422	enolase (2-phosphoglycerate dehydratase)(2-phospho-D-glycerate hydro-lyase)
1086	4586	1036159	1036016	144	PIR B72477	Aeropyrum pernix K1 APE2459	68 0	58 0	41	hypothetical protein
1087	4587	1036316	1036855	540	pir C70623	Mycobacterium tuberculosis H37Rv Rv1024	31 9	55 0	191	hypothetical protein
1088	4588	1036900	1037445	546	pir D70623	Mycobacterium tuberculosis H37Rv Rv1025	59 5	77 8	153	hypothetical protein
1089	4589	1037448	1038410	963	sp GPPA_ECOLI	Escherichia coli gppA	25 2	55 0	329	guanosine pentaphosphatase or exopolyphosphatase
1090	4590	1037461	1036498	984						
1091	4591	1039650	1038721	930	sp THD2_ECOLI	Escherichia coli tdcB	30 3	64 7	314	threonine dehydratase
1092	4592	1039783	1039977	195						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1093	4593	1039996	1040325	330						
1094	4594	1040494	1040682	189	pir B72287	Thermotoga maritima MSB8	46.3	74.1	56	hypothetical protein
1095	4595	1040925	1041917	993	sp RHAR_ECOLI	Escherichia coli rhaR	24.8	55.8	242	transcription activator of L-rhamnose operon
1096	4596	1042027	1042842	816	pir F70893	Mycobacterium tuberculosis H37Rv Rv1072	57.8	80.1	282	hypothetical protein
1097	4597	1043236	1042850	387						
1098	4598	1043747	1043298	450	gp SCF55_39	Streptomyces coelicolor A3(2) SCF55.39	30.0	57.1	140	hypothetical protein
1099	4599	1044295	1043774	522	sp GREA_ECOLI	Escherichia coli greA	35.0	60.1	143	transcription elongation factor
1100	4600	1044959	1044477	483	pir G70894	Mycobacterium tuberculosis H37Rv Rv1081c	34.3	72.1	140	hypothetical protein
1101	4601	1045158	1046030	873	pir S44952	Streptomyces lincolnensis lmbE	31.7	56.3	300	lincomycin-production
1102	4602	1046073	1046390	318						
1103	4603	1046610	1047707	1098	sp AROG_CORGL	Corynebacterium glutamicum aroG	99.2	99.5	367	3-deoxy-D-arabino-heptulosonate-7-phosphate synthase
1104	4604	1047452	1046820	633						
1105	4605	1047827	1048501	675	sp YARF_CORGL	Corynebacterium glutamicum CCRC18310	96.0	97.3	97	hypothetical protein or undecaprenyl pyrophosphate synthetase
1106	4606	1048356	1048529	174	SP YARF_CORGL	Corynebacterium glutamicum (Brevibacterium flavum)	100.0	100.0	28	hypothetical protein
1107	4607	1048525	1049043	519						
1108	4608	1049385	1049068	318						
1109	4609	1050362	1049427	936	sp COAA_ECOLI	Escherichia coli coaA	53.9	79.9	308	pantothenate kinase
1110	4610	1050624	1051925	1302	gsp R97745	Brevibacterium flavum MJ-233 glyA	99.5	100.0	434	serine hydroxymethyl transferase
1111	4611	1052021	1053880	1860	sp PABS_STRGR	Streptomyces griseus pabS	47.6	70.1	696	p-aminobenzoic acid synthase
1112	4612	1053880	1054602	723						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1113	4613	1054859	1055722	864						
1114	4614	1055032	1054640	393						
1115	4615	1055783	1056319	537	gp AC1504_1	Alcaligenes faecalis steR	30 3	58 8	165	phosphinothricin resistance protein
1116	4616	1057200	1056322	879	sp YBGK_ECOLI	Escherichia coli ybgK	30 3	59 0	300	hypothetical protein
1117	4617	1057573	1058628	1056						
1118	4618	1057868	1057200	669	sp YBGJ_ECOLI	Escherichia coli ybgJ	37 8	57 8	225	hypothetical protein
1119	4619	1058598	1057843	756	sp LAMB_EMENI	Emericella nidulans lamB	30 8	52 2	276	lactam utilization protein
1120	4620	1059214	1058624	591	sp YCSH_BACSU	Bacillus subtilis ycsH	40 6	81 2	165	hypothetical membrane protein
1121	4621	1059218	1059889	672						
1122	4622	1059360	1059962	603						
1123	4623	1060112	1060792	681	sp YDHC_BACSU	Bacillus subtilis ydhC	26 0	63 2	204	transcriptional regulator
1124	4624	1060869	1062146	1278						
1125	4625	1062209	1062211	1419	sp FUMH_RAT	Rattus norvegicus (Rat) fumH	52 0	79 4	456	fumarate hydratase precursor
1126	4625	1063936	1064424	489	gp AF048079_1	Rhodococcus erythropolis IGTS8 dszD	32 7	65 4	159	NADH dependent FMN oxydoreductase
1127	4627	1064738	1064478	261						
1128	4628	1065200	1064754	447						
1129	4629	1065867	1065304	564	gp SCAH10_16	Streptomyces coelicolor A3(2) StAH10 16	55 4	81 0	184	reductase
1130	4630	1066083	1065870	1489	sp SOXA_RHOSO	Rhodococcus sp IGTS8 soxA	39 1	67 7	443	dibenzothiophene desulfurization enzyme A
1131	4631	1067570	1068649	1080	sp SOXC_RHOSO	Rhodococcus sp IGTS8 soxC	25 8	51 3	372	dibenzothiophene desulfurization enzyme C (DBT sulfur dioxygenase)
1132	4632	1068649	1069845	1197	sp SOXC_RHOSO	Rhodococcus sp IGTS8 soxC	28 9	61 6	391	dibenzothiophene desulfurization enzyme C (DBT sulfur dioxygenase)
1133	4633	1069692	1068913	780						
1134	4634	1069808	1069119	690						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
1135	4635	1069959	1071134	1176	gp ECO237695_3	Escherichia coli K12 ssuD	45.3	73.1	397	FMNH2-dependent aliphatic sulfonate monooxygenase
1136	4636	1072441	1071479	963	sp GLPY_ECOLI	Escherichia coli K12 glpY	44.3	75.7	325	glycerol metabolism
1137	4637	1072676	1073245	570	pir B70997	Mycobacterium tuberculosis H37Rv Rv1100	27.5	56.4	211	hypothetical protein
1138	4638	1075241	1073340	1902	pir H70062	Bacillus subtilis yvmD	31.3	66.1	227	hypothetical protein
1139	4639	1075357	1075641	285						
1140	4640	1075553	1075329	225	gp SCH24_37	Streptomyces coelicolor A3(2) SCH24.37	36.6	78.1	82	transmembrane efflux protein
1141	4641	1075909	1075667	243	sp EX7S_ECOLI	Escherichia coli K12 MG1655 xseB	40.3	67.7	62	exodeoxyribonuclease small subunit
1142	4642	1077183	1075933	1251	sp EX7L_ECOLI	Escherichia coli K12 MG1655 xseA	30.0	55.6	466	exodeoxyribonuclease large subunit
1143	4643	1077297	1078271	975	sp LYTB_ECOLI	Escherichia coli K12 lytB	50.2	78.8	311	penicillin tolerance
1144	4644	1077734	1077336	429	GSP Y75421	Neisseria gonorrhoeae	33.0	47.0	131	polypeptides predicted to be useful antigens for vaccines and diagnostics
1145	4645	1079146	1078319	828						
1146	4646	1080540	1079221	1320	sp PERM_ECOLI	Escherichia coli K12 perM	26.3	63.9	338	permease
1147	4647	1080965	1080786	180						
1148	4648	1082708	1080972	1737	sp NTPR_RAT	Rattus norvegicus (Rat) SLC6A7 ntpR	30.3	61.4	552	sodium-dependent proline transporter
1149	4649	1084184	1082961	1224	sp CSP1_CORGL	Corynebacterium glutamicum (Brevibacterium flavum) ATCC 17965 csp1	29.9	60.0	412	major secreted protein PS1 protein precursor
1150	4650	1084380	1085462	1083	sp YYAF_BACSU	Bacillus subtilis yyaF	70.1	88.6	361	GTP-binding protein
1151	4651	1085791	1086087	297	sp VAPI_BACNO	Dichelobacter nodosus intA	57.3	80.0	75	virulence-associated protein
1152	4652	1086096	1086917	822	sp OTCA_PSEAE	Pseudomonas aeruginosa argF	29.6	58.8	301	ornithine carbamoyltransferase
1153	4653	1087544	1087044	501	sp YKKB_BACSU	Bacillus subtilis 168 ykkB	39.2	69.9	143	hypothetical protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1154	4654	1088293	1087664	630	gp AF013288_1	Mus musculus RDH4	33 8	60 6	198	9-cis retinol dehydrogenase or oxidoreductase
1155	4655	1089740	1088535	1206	sp YIS1_STRCO	Streptomyces coelicolor SC3C8 10	42 2	73 0	396	transposase/integrase (IS110)
1156	4656	1090175	1093216	3042	sp YEGE_ECOLI	Escherichia coli K12 yegE	23 0	52 2	1153	hypothetical membrane protein
1157	4657	1093929	1094693	765	sp NODC_RHIME	Rhizobium meliloti nodC	22 8	47 1	259	N-acetylglucosaminyltransferase
1158	4658	1094693	1094911	219						
1159	4659	1095052	1095384	333						
1160	4660	1095677	1095387	291	pir S43613	Corynebacterium glutamicum ATCC 31831	82 5	93 8	97	transposase (insertion sequence IS31831)
1161	4661	1096093	1095719	375	pir JC4742	Corynebacterium glutamicum (Brevibacterium lactofermentum) ATCC 13869	79 2	94 4	125	transposase
1162	4662	1096331	1096188	144	pir JC4742	Corynebacterium glutamicum (Brevibacterium lactofermentum) ATCC 13869	87 5	95 8	48	transposase
1163	4663	1096471	1096331	141						
1164	4664	1097111	1096746	366						
1165	4665	1097229	1097726	498						
1166	4666	1097750	1098592	843	sp MORA_PSEPU	Pseudomonas putida M10 norA	37 5	66 3	264	oxidoreductase or morpyine-6-dehydrogenase (naloxone reductase)
1167	4667	1098609	1098929	321	sp DC4C_ACICA	Acinetobacter calcoaceticus dc4c	33 3	63 9	108	4-carboxymuconolactone decarboxlyase
1168	4668	1099088	1099750	663						
1169	4669	1099209	1099015	195						
1170	4670	1099768	1099115	654	gp AF058302_19	Streptomyces roseofulvus frnS	34 9	66 4	146	frenolicin gene cluster protein involved in frenolicin biosynthetic

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1171	4671	1099917	1101653	1737	gp SPU59234_3	Synechococcus sp PCC 7942 accC	48.1	78.5	563	biotin carboxylase
1172	4672	1102043	1102639	597						
1173	4673	1102695	1103192	498						
1174	4674	1103180	1103524	345						
1175	4675	1103951	1104103	153						
1176	4676	1104923	1105561	639						
1177	4677	1106058	1104103	1956	sp YT15_MYCTU	Mycobacterium tuberculosis H37Rv Rv0959	57.9	80.3	655	hypothetical protein
1178	4678	1107381	1106086	1296	sp BCHI_RHOSH	Rhodobacter sphaeroides ATCC 17023 bchI	27.7	52.6	329	magnesium chelatase subunit
1179	4679	1107560	1108201	642	gp AMJ73808_1	Amycolatopsis methanolica pgm	33.8	62.5	160	2,3-PDG dependent phosphoglycerate mutase
1180	4680	1108201	1108905	705	pir A70577	Mycobacterium tuberculosis H37Rv Rv2133c	38.2	60.7	262	hypothetical protein
1181	4681	1108993	1109754	762	gp STMBCPA_1	Streptomyces hygroscopicus SF1293 BcpA	29.4	59.3	248	carboxyphosphonoenolpyruvate phosphonomutase
1182	4682	1109792	1111432	1641	sp TLRC_STRFR	Streptomyces fradiae tlrC	31.7	54.1	593	tyrosin resistance ATP-binding protein
1183	4683	1111820	1111425	396	sp Y923C_MYCTU	Mycobacterium tuberculosis H37Rv Rv2923c	29.4	66.9	136	hypothetical protein
1184	4684	1111889	1112230	342	sp PHNA_ECOLI	Escherichia coli K12 MG1655 phnA	55.0	82.0	111	alkylphosphonate uptake protein
1185	4685	1112957	1112484	474	sp YXAD_BACSU	Bacillus subtilis 168 yxaD	32.1	62.7	134	transcriptional regulator
1186	4686	1113102	1114319	1218	gp SPN7367_1	Streptococcus pneumoniae pmrA	22.6	59.4	367	multi-drug resistance efflux pump
1187	4687	1114486	1115793	1308	pir S43613	Corynebacterium glutamicum (Brevibacterium lactofermentum) ATCC 31831	99.5	99.8	436	transposase (insertion sequence IS31831)

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
1188	4688	1116905	1115832	1074	gp RFAJ3152_2	Ruminococcus flavefaciens cysteine desulphurase gene	43.9	73.4	376	cysteine desulphurase
1189	4689	1117744	1116908	837	sp NADC_MYCTU	Mycobacterium tuberculosis	42.1	68.9	283	nicotinate nucleotide pyrophosphorylase
1190	4690	1118932	1117751	1182	pir E69663	Bacillus subtilis nadA	49.3	77.6	361	quinolinate synthetase A
1191	4691	1119727	1119086	642	gp SC5B8_7	Streptomyces coelicolor SC5B8.07	37.0	60.9	235	DNA hydrolase
1192	4692	1120205	1120804	600	gp AE001961_5	Deinococcus radiodurans R1 DR1112	23.4	54.7	192	hypothetical membrane protein
1193	4693	1121432	1120833	600	gp SC3A7_8	Streptomyces coelicolor SC3A7.08	36.0	66.4	214	hypothetical protein
1194	4694	1121809	1121468	342	sp YBDF_ECOLI	Escherichia coli K12 MG1655 ybdF	41.7	74.1	108	hypothetical protein
1195	4695	1122606	1121818	789	gp AAA21740_1	Escherichia coli K12 lplA	30.1	60.7	216	lipoate-protein ligase A
1196	4696	1123051	1123461	411	sp PHNB_ECOLI	Escherichia coli K12 phnB	29.7	60.8	148	alkylphosphonate uptake protein and C-P lyase activity
1197	4697	1124826	1123534	1293	sp PCAK_PSEPU	Pseudomonas putida pcaK	28.8	64.3	420	transmembrane transport protein or 4 hydroxybenzoate transporter
1198	4698	1126020	1124836	1185	sp PHHY_PSEAE	Pseudomonas aeruginosa phhy	40.8	68.6	395	p-hydroxybenzoate hydroxylase (4-hydroxybenzoate 3-monooxygenase)
1199	4699	1126422	1127009	588	pir A69859	Bacillus subtilis 168 ykoE	36.7	69.6	191	hypothetical membrane protein
1200	4700	1127013	1128350	1338	sp YJJK_ECOLI	Escherichia coli yjjK	24.8	47.6	532	ABC transporter ATP-binding protein
1201	4701	1128350	1129102	753	pir G69858	Bacillus subtilis 168 ykoC	25.6	61.6	250	hypothetical membrane protein
1202	4702	1129102	1129632	531						
1203	4703	1129655	1130704	1050	sp CHAA_ECOLI	Escherichia coli chaA	33.3	69.0	339	Ca2+/H+ antiporter ChaA
1204	4704	1130721	1131428	708	pir C75001	Pyrococcus abyssi Orsay PAB1341	28.4	57.6	236	hypothetical protein
1205	4705	1132123	1131401	723	sp YWAF_BACSU	Bacillus subtilis ywaF	27.6	61.1	221	hypothetical membrane protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1206	4706	1134472	1132133	2340	sp UVRA_THETH	Thermus thermophilus unrA	35 5	58.7	946	excinuclease ABC subunit A
1207	4707	1134561	1135055	495	sp TPX_MYCTU	Mycobacterium tuberculosis H37Rv tpx	57 3	81.7	164	thioredoxin peroxidase
1208	4708	1135476	1135691	216						
1209	4709	1136833	1135058	1776						
1210	4710	1137891	1136938	954	sp YEDI_ECOLI	Escherichia coli yedL	39 9	72.0	318	hypothetical membrane protein
1211	4711	1137960	1138859	900	gp SCF76_2	Streptomyces coelicolor A3(2)	34 0	49 0	282	oxidoreductase or thiamin biosynthesis protein
1212	4712	1138880	1139245	366						
1213	4713	1139196	1139492	297						
1214	4714	1139357	1139617	261						
1215	4715	1140021	1139635	387						
1216	4716	1140861	1140028	834	sp CTR2_PENVA	Penaeus vannamei	28 8	51 3	271	chymotrypsin BII
1217	4717	1141245	1140901	345	sp ARC2_ECOLI	Escherichia coli	43 2	72 1	111	arsenate reductase (arsenical pump modifier)
1218	4718	1141273	1142472	1200	sp YYAD_BACSU	Bacillus subtilis yyaD	23 5	62 4	340	hypothetical membrane protein
1219	4719	1143015	1142479	537	pir F70559	Mycobacterium tuberculosis H37Rv Rv1632c	43 5	71.4	147	hypothetical protein
1220	4720	1143739	1143026	714	pir F70555	Mycobacterium tuberculosis H37Rv Rv1157c	35.8	62 9	221	hypothetical protein
1221	4721	1144118	1146028	1911	sp TYPA_ECOLI	Escherichia coli K12 typA	46.3	76.7	614	GTP-binding protein (tyrosine phsphorylated protein A)
1222	4722	1146097	1147602	1506	pir F70874	Mycobacterium tuberculosis H37Rv Rv1166	27.9	54 9	506	hypothetical protein
1223	4723	1147592	1148461	870	pir B70875	Mycobacterium tuberculosis H37Rv Rv1170	38.7	61.9	315	hypothetical protein
1224	4724	1148445	1148882	438						
1225	4725	1148953	1149267	315	sp FER_STRGR	Streptomyces griseus fer	78.6	91.3	103	ferredoxin [4Fe-4S]

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (aa)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (aa)	Function
1226	4726	1149279	1150379	1101	sp AAT_BACSP	Bacillus sp strain YM-2 aat	25 9	52 9	397	aspartate aminotransferase
1227	4727	1150408	1151028	621						
1228	4728	1151186	1152370	1185						
1229	4729	1153063	1152373	891	gp CGAJ4934_1	Corynebacterium glutamicum ATCC 13032 dapD	100 0	100 0	229	tetrahydrodipicolinate succinylase or succinylation of piperidine-2,6-dicarboxylate
1230	4730	1156537	1155875	663						
1231	4731	1158062	1157669	768	pir S60064	Corynebacterium glutamicum ATCC 13032 orf2	100 0	100 0	211	hypothetical protein
1232	4732	1157694	1158524	831	gp SCP8_4	Streptomyces coelicolor A3(2) dhpS	59 0	69 0	273	dihydropteroate synthase
1233	4733	1158524	1159252	729	gp MLU15180_14	Mycobacterium leprae u1756l	45 7	73 1	245	hypothetical protein
1234	4734	1159267	1159572	306	pir G70609	Mycobacterium tuberculosis H37Rv Rv1209	31 3	67 7	99	hypothetical protein
1235	4735	1159635	1159799	165	gsp W32443	Mycobacterium tuberculosis	72 3	91 5	47	antigen TbAAMK, useful in vaccines for prevention or treatment of tuberculosis
1236	4736	1159865	1160728	864	sp MYRA_MICGR	Micromonospora griseorubida myrA	39 2	67 8	286	mycinamicin resistance gene
1237	4737	1162231	1160738	1494	sp SCRB_PEDPE	Pediococcus pentosaceus scrB	23 5	51 0	524	sucrose 6 phosphate hydrolase
1238	4738	1163605	1162379	1227	sp GLCA_ECOLI	Escherichia coli K12 MG1655 glgA	24 7	51 3	433	ADPglucose--starch(bacterial glycogen) glucosyltransferase
1239	4739	1163702	1164916	1215	sp GLGC_STRCO	Streptomyces coelicolor A3(2) glgC	61 0	81 8	400	glucose-1-phosphate adenylyltransferase
1240	4740	1165612	1164974	639	sp MDMC_STRMY	Streptomyces mycarofaciens MdmC	25 8	62 4	93	methyltransferase
1241	4741	1165746	1166384	639	sp RPOE_ECOLI	Escherichia coli rpoE	27 3	57 2	194	RNA polymerase sigma factor (sigma-24), heat shock and oxidative stress
1242	4742	1166376	1167067	492						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (aa)	nitial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (aa)	Function
1243	4743	1167110	1167577	468	pir:C70508	Mycobacterium tuberculosis H37Rv Rv1224	45.5	73.2	112	hypothetical protein
1244	4744	1168711	1167587	1125	sp:MRP_ECOLI	Escherichia coli mrp	43.6	72.0	257	ATPase
1245	4745	1169325	1168747	579	pir:B70509	Mycobacterium tuberculosis H37Rv Rv1231c	60.4	83.8	154	hypothetical protein
1246	4746	1170610	1169321	1290	pir:C70509	Mycobacterium tuberculosis H37Rv Rv1232c	49.8	77.0	434	hypothetical protein
1247	4747	1170672	1171187	516	pir:A70952	Mycobacterium tuberculosis H37Rv Rv1234	57.9	87.1	140	hypothetical protein
1248	4748	1171206	1171871	666						
1249	4749	1172462	1171869	594						
1250	4750	1176271	1172501	3771	prf:2306367A	Corynebacterium glutamicum AJ12036 odhA	99.4	99.8	1257	2-oxoglutarate dehydrogenase
1251	4751	1180048	1176308	3741	sp:MDR2_CRIGR	Cricetulus griseus (Chinese hamster) MDR2	28.8	60.4	1288	ABC transporter or multidrug resistance protein 2 (P-glycoprotein 2)
1252	4752	1180937	1180121	717	pir:H70953	Mycobacterium tuberculosis H37Rv Rv1249c	31.7	72.1	240	hypothetical protein
1253	4753	1181675	1180872	804	sp:AROE_ECOLI	Escherichia coli aroE	25.5	61.2	255	sh.kimate dehydrogenase
1254	4754	1181993	1183603	1611	sp:PNBA_BACSU	Bacillus subtilis pnbA	35.7	64.7	501	para-nitrobenzyl esterase
1255	4755	1183607	1184257	651						
1256	4756	1184280	1185155	876						
1257	4757	1185742	1185218	525						
1258	4758	1185825	1187039	1215	sp:TCR1_ECOLI	Escherichia coli transposon Tn1721 tetA	27.1	61.4	409	tetracycline resistance protein
1259	4759	1187043	1188389	1347	sp:TCMA_STRGA	Streptomyces glaucescens tcmA	32.4	64.2	444	metabolite export pump of tetracenomycin C resistance
1260	4760	1189822	1190526	705						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (aa)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (aa)	Function
1261	4761	1190622	1188388	2235	pir S57636	Catharanthus roseus metE	45.2	72.2	774	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase
1262	4762	1191087	1191542	456						
1263	4763	1192410	1193807	1398	gsp Y29930	Nocardia asteroides strain KGB1	55.2	79.5	444	thiophene biotransformation protein
1264	4764	1193867	1194190	324						
1265	4765	1194165	1195109	945						
1266	4766	1195916	1195125	792						
1267	4767	1195974	1197620	1647						
1268	4768	1197624	1197815	192						
1269	4769	1199543	1197990	1554	sp CYDC_ECOLI	Escherichia coli K12 MG1655 cydC	28.7	63.5	526	ABC transporter
1270	4770	1201075	1199543	1533	sp CYDD_ECOLI	Escherichia coli K12 MG1655 cydD	29.4	58.4	551	ABC transporter
1271	4771	1202088	1201090	999	gp AB035066_2	Corynebacterium glutamicum (Brevibacterium lactofermentum) cydB	92.0	93.0	333	cytochrome bd type menaquinol oxidase subunit II
1272	4772	1203632	1202094	1539	gp AB035066_1	Corynebacterium glutamicum (Brevibacterium lactofermentum) cydA	99.6	99.0	512	cytochrome bd type menaquinol oxidase subunit I
1273	4773	1206180	1203916	2265	sp YEIH_ECOLI	Escherichia coli K12 MG1655 yejH	26.4	55.0	402	helicase
1274	4774	1206316	1206657	342						
1275	4775	1207223	1206831	393	sp MUTT_PROVU	Proteus vulgaris mutT	36.9	65.6	98	mutator mutT protein ((7,8 dihydro 8 oxoguanine triphosphatase)(8 oxo dGTPase)(dGTP pyrophosphohydrolase)
1276	4776	1207374	1208139	765						
1277	4777	1209615	1208212	1404	sp PROY_SALTY	Salmonella typhimurium proY	51.3	85.0	433	proline-specific permease

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
1278	4778	1209934	1212129	2196	sp:DEAD_KLEPN	Klebsiella pneumoniae CG43 DEAD box ATP-dependent RNA helicase deaD	48.1	74.3	643	DEAD box ATP-dependent RNA helicase
1279	4779	1213115	1212429	687	prf:2323363BT	Mycobacterium leprae B1308_C2_181	24.7	47.4	247	bacterial regulatory protein, tetR family
1280	4780	1213200	1214858	1659	sp:PCPB_FLAS3	Sphingomonas flava pcpB	24.5	47.7	595	pentachlorophenol 4-monooxygenase
1281	4781	1214871	1215938	1068	sp:CLCE_PSESB	Pseudomonas sp. B13 clcE	40.4	72.0	354	maleylacetate reductase
1282	4782	1215952	1216836	885	sp:CATA_ACICA	Acinetobacter calcoaceticus catA	30.6	59.4	278	catechol 1,2-dioxygenase
1283	4783	1217374	1216904	471						
1284	4784	1217982	1217443	540	pir:A70672	Mycobacterium tuberculosis H37Rv Rv2972c	31.9	58.4	185	hypothetical protein
1285	4785	1219895	1222996	3102	sp:SNF2_YEAST	Saccharomyces cerevisiae SNF2	24.9	55.4	878	transcriptional regulator
1286	4786	1222995	1221841	1065						
1287	4787	1222980	1223843	858	gp:SCO007731_6	Streptomyces coelicolor A3(2) orfZ	29.6	56.2	203	hypothetical protein
1288	4788	1223887	1225059	1173	pir:E70755	Mycobacterium tuberculosis H37Rv Rv1277	39.2	67.3	395	phosphoesterase
1289	4789	1225066	1227693	2628	sp:Y084_MYCTU	Mycobacterium tuberculosis H37Rv Rv1278	29.7	59.6	915	hypothetical protein
1290	4790	1227587	1227282	306						
1291	4791	1227657	1227340	318						
1292	4792	1227363	1228636	774	gp:AB029896_1	Petroleum-degrading bacterium HD-1 hde	37.3	64.6	220	esterase or lipase
1293	4793	1228718	1229095	378						
1294	4794	1229150	1229935	786						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1295	4795	1229716	1229180	537	sp:ATOE_ECOLI	Streptomyces coelicolor SC1C2 14c atoE	37 7	69 7	122	short-chain fatty acids transporter
1296	4796	1229995	1230480	486	sp:RECS_ERWCH	Erwinia chrysanthemi recS	24 7	56 6	166	regulatory protein
1297	4797	1230610	1230831	222						
1298	4798	1231432	1230914	519						
1299	4799	1231730	1232479	750	sp:FNR_ECOLI	Escherichia coli K12 MG1655 fnr	25 0	57 9	228	fumarate (and nitrate) reduction regulatory protein
1300	4800	1232603	1232836	234	sp:MERP_SHEPU	Shewanella putrefaciens merP	33 3	66 7	81	mercuric transort protein periplasmic component precursor
1301	4801	1233007	1234881	1875	sp:ATZN_ECOLI	Escherichia coli K12 MG1655 atzN	38 0	70 6	605	zinc-transporting ATPase Zn(II)-translocating P-type ATPase
1302	4802	1234983	1235612	630	sp:RELA_VIBSS	Vibrio sp S14 relA	32 9	58 4	137	GTP pyrophosphokinase (ATP GTP 3'-pyrophosphotransferase) (ppGpp synthetase I)
1303	4803	1238125	1236545	1581	gsp:R80504	Streptomyces lividans tap	26 6	49 3	601	tripeptidyl aminopeptidase
1304	4804	1242156	1241554	603						
1305	4805	1242275	1242156	120						
1306	4806	1243621	1243728	108	GSP:P61449	Corynebacterium glutamicum	95 0	98 0	24	homoserine dehydrogenase
1307	4807	1245201	1243942	1260						
1308	4808	1245532	1244843	690						
1309	4809	1246496	1245720	777	sp:NARI_BACSU	Bacillus subtilis narI	45 0	69 6	220	nitrate reductase gamma chain
1310	4810	1247239	1246508	732	sp:NARJ_BACSU	Bacillus subtilis narJ	30 3	63 4	175	nitrate reductase delta chain
1311	4811	1248791	1247199	1593	sp:NARH_BACSU	Bacillus subtilis narH	56 6	83 4	505	nitrate reductase beta chain
1312	4812	1249851	1250444	594	PIR:D72603	Aeropyrum pernix K1 APE1291	36 0	48 0	137	hypothetical protein
1313	4813	1251545	1251817	273	PIR:B72603	Aeropyrum pernix K1 APE1289	36 0	55 0	83	hypothetical protein
1314	4814	1252537	1248794	3744	sp:NARG_BACSU	Bacillus subtilis narG	46 9	73 8	1271	nitrate reductase alpha chain
1315	4815	1253906	1252557	1350	sp:NARK_ECOLI	Escherichia coli K12 narK	32 8	67 9	461	nitrate extrusion protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
1316	4616	1254140	1254634	489	sp CNX1_ARATH	Arabidopsis thaliana CV cnx1	32.5	65.0	157	molybdopterin biosynthesis cnx1 protein (molybdenum cofactor biosynthesis enzyme cnx1)
1317	4617	1256602	1254737	1866	sp PRTS_SERMA	Serratia marcescens strain IFO-3046 prtS	21.1	45.9	738	extracellular serine protease precurosor
1318	4618	1257067	1257750	684						
1319	4619	1257858	1256851	1008	sp Y0D3_MYCTU	Mycobacterium tuberculosis H37Rv Rv1841c	30.8	62.6	334	hypothetical membrane protein
1320	4620	1259265	1257865	1401	sp Y0D2_MYCTU	Mycobacterium tuberculosis H37Rv Rv1842c	31.6	60.2	472	hypothetical membrane protein
1321	4621	1259989	1259429	561	gp PPU242852_2	Pseudomonas putida mobA	27.5	52.3	178	molybdopterin guanine dinucleotide synthase
1322	4622	1261201	1259993	1209	sp MOEA_ECOLI	Mycobacterium tuberculosis H37Rv Rv0438c moeA	32.8	58.2	366	molybdoptein biosynthesis protein
1323	4623	1262819	1261688	1131	sp CNX2_ARATH	Arabidopsis thaliana cnx2	51.4	73.7	354	molybdopterin biosynthsisi protein Moybdenume (mosybdenum cofastor biosythesis enzyme)
1324	4624	1264010	1262886	1125	sp ALKK_PSEOL	Pseudomonas oleovorans	36.7	65.7	572	edium-chain fatty acid--CoA ligase
1325	4625	1265142	1267427	2286	sp RHO_MICLU	Micrococcus luteus rho	50.7	73.8	753	Rho factor
1326	4626	1265665	1266267	603						
1327	4627	1266306	1265611	696						
1328	4628	1266449	1265427	1023						
1329	4629	1267430	1268503	1074	sp RF1_ECOLI	Escherichia coli K12 RF-1	41.9	71.9	363	peptide chain release factor 1
1330	4630	1268507	1269343	837	sp HEMK_ECOLI	Escherichia coli K12	31.1	57.9	280	protoporphyrinogen oxidase
1331	4631	1269040	1268267	774						
1332	4632	1269396	1270043	648	sp Y001_MYCTU	Mycobacterium tuberculosis H37Rv Rv1301	62.3	86.0	215	hypothetical protein
1333	4633	1270047	1271192	1146	sp RFE_ECOLI	Escherichia coli K12 rfe	31.1	58.4	322	undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1334	4834	1271213	1271698	486						
1335	4835	1271871	1272119	249	GPU AB046112_1	Corynebacterium glutamicum atpI	98.0	99.0	80	hypothetical protein
1336	4836	1272340	1273149	810	sp ATP6_ECOLI	Escherichia coli K12 atpB	24.1	56.7	245	ATP synthase chain a (protein 6)
1337	4837	1273286	1273525	240	sp ATPL_STRLI	Streptomyces lividans atpL	54.9	85.9	71	H+-transporting ATP synthase lipid binding protein ATP synthase C chane
1338	4838	1273559	1274122	564	sp ATPF_STRLI	Streptomyces lividans atpF	27.8	66.9	151	H+-transporting ATP synthase chain b
1339	4839	1274131	1274943	813	sp ATPD_STRLI	Streptomyces lividans atpD	34.3	67.2	274	H+-transporting ATP synthase delta chain
1340	4840	1274975	1276648	1674	sp ATPA_STRLI	Streptomyces lividans atpA	66.9	88.4	516	H+-transporting ATP synthase alpha chain
1341	4841	1276708	1277682	975	sp ATPG_STRLI	Streptomyces lividans atpG	46.3	76.6	320	H+-transporting ATP synthase gamma chain
1342	4842	1277688	1279136	1449	sp ATPB_CORGL	Corynebacterium glutamicum AS019 atpB	99.8	100.0	483	H+-transporting ATP synthase beta chain
1343	4843	1279151	1279522	372	sp ATPE_STRLI	Streptomyces lividans atpE	41.0	73.0	122	H+-transporting ATP synthase epsilon chain
1344	4844	1279770	1280240	471	sp Y02W_MYCTU	Mycobacterium tuberculosis H37Rv Rv1312	38.6	67.4	132	hypothetical protein
1345	4845	1280270	1280959	690	sp Y036_MYCTU	Mycobacterium tuberculosis H37Rv Rv1321	70.0	85.7	230	hypothetical protein
1346	4846	1280967	1281251	285	GP SC26G5_35	Streptomyces coelicolor A3(2)	45.0	56.0	95	putative ATP/GTP binding protein
1347	4847	1281714	1281262	453	sp YQJC_BACSU	Bacillus subtilis yqjC	35.8	68.7	134	hypothetical protein
1348	4848	1281794	1282105	312	sp YC20_MYCTU	Mycobacterium tuberculosis H37Rv Rv1898	54.5	79.2	101	hypothetical protein
1349	4849	1282194	1283114	921	sp YD24_MYCTU	Mycobacterium tuberculosis H37Rv Rv1324	37.9	71.4	301	thioredoxin

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1350	4850	1283324	1284408	1143	gp ECO237695_3	Escherichia coli K12 ssuD	50.3	74.3	366	FMNH2 dependent aliphatic sulfonate monooxygenase
1351	4851	1284517	1285284	768	sp SSUC_ECOLI	Escherichia coli K12 ssuC	40.8	75.8	240	alphatic sulfonates transport permease protein
1352	4852	1285302	1286030	729	sp SSUB_ECOLI	Escherichia coli K12 ssuB	50.4	72.8	228	alphatic sulfonates transport permease protein
1353	4853	1286043	1286999	957	sp SSUA_ECOLI	Escherichia coli K12 ssuA	35.1	62.1	311	sulfonate binding protein precursor
1354	4854	1289473	1287281	2193	sp GLGB_ECOLI	Mycobacterium tuberculosis H37Rv Rv1326c glgB	46.1	72.7	710	1,4-alpha-glucan branching enzyme (glycogen branching enzyme)
1355	4855	1291007	1289514	1494	sp AMY3_DICTH	Dictyoglomus thermophilum amyC	22.9	50.5	467	alpha-amylase
1356	4856	1291025	1291373	348						
1357	4857	1291609	1292577	879	sp FEPC_ECOLI	Escherichia coli K12 fepC	31.8	87.6	211	ferric enterobactin transport ATP-binding protein or ABC transport ATP-binding protein
1358	4858	1293222	1294025	804	pir C70860	Mycobacterium tuberculosis H37Rv Rv3040c	39.6	68.5	260	hypothetical protein
1359	4859	1294151	1295206	1056	p r H70859	Mycobacterium tuberculosis H37Rv Rv3037c	43.1	70.0	367	hypothetical protein
1360	4860	1295047	1294436	612						
1361	4861	1295435	1296220	786	sp FIXA_RHIME	Rhizobium meliloti fixA	31.2	64.8	244	electron transfer flavoprotein beta-subunit
1362	4862	1296253	1297203	951	sp FIXB_RHIME	Rhizobium meliloti fixB	33.1	61.8	335	electron transfer flavoprotein alpha subunit for various dehydrogenases
1363	4863	1297479	1297093	615						
1364	4864	1297212	1298339	1128	sp NIFS_AZOVI	Azotobacter vinelandii nifS	35.2	67.7	375	nitrogenase cofactor sythesis protein
1365	4865	1298653	1298342	312						
1366	4866	1300145	1299000	1146	sp Y4ME_RHISN	Rhizobium sp. NGR234 plasmid pNGR234a y4mE	29.5	55.7	397	hypothetical protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1367	4867	1300369	1300145	225	sp Y4MF_RHISN	Rhizobium sp NGR234 plasmid pNGR234a Y4mF	47 5	76 3	59	transcriptional regulator
1368	4868	1300552	1301055	504	sp YHBS_ECOLI	Escherichia coli K12 MG1655 yhbS	34 8	55 3	181	acetyltransferase
1369	4869	1301929	1300988	942						
1370	4870	1303123	1301975	1149						
1371	4871	1303299	1303694	396						
1372	4872	1303829	1304923	1095	pir C70858	Mycobacterium tuberculosis H37Rv Rv3024c	61 8	80 9	361	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
1373	4873	1304536	1303883	654						
1374	4874	1304932	1305921	990	pir B70857	Mycobacterium tuberculosis H37Rv Rv3015c	33 7	66 0	332	hypothetical protein
1375	4875	1307384	1305924	1461	sp TCMA_STRGA	Streptomyces glaucescens tcmA	30 2	65 8	500	tetracenomycin C resistance and export protin
1376	4876	1308196	1307462	735						
1377	4877	1308330	1310369	2040	sp DNLJ_RHOMR	Rhodothermus marinus dnlJ	42 8	70 6	677	DNA ligase (polydeoxyribonucleotide synthase [NAD+]
1378	4878	1311097	1310435	663	pir H70856	Mycobacterium tuberculosis H37Rv Rv3013	40 0	70 9	220	hypothetical protein
1379	4879	1311320	1311616	297	sp GATC_STRCO	Streptomyces coelicolor A3(2) gatC	53 0	64 0	97	glutamyl-tRNA(Gln) amidotransferase subunit C
1380	4880	1311625	1313115	1491	sp GATA_MYCTU	Mycobacterium tuberculosis H37Rv gatA	74 0	83 0	484	glutamyl-tRNA(Gln) amidotransferase subunit A
1381	4881	1313270	1314118	849	sp VIUB_VIBVU	Vibrio vulnificus viuB	28 1	54 0	263	vibriobactin utilization protein / iron chelator utilization protein
1382	4882	1314775	1314479	306	gp SCE6_24	Streptomyces coelicolor A3(2) SCE6 24	46 9	79 2	96	hypothetical membrane protein
1383	4883	1315013	1316083	1071	sp PFP_AMYME	Amycolatopsis methanolica pfp	54 8	77 9	358	pyrophosphate--fructose 6 phosphate 1-phosphotransferase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
1384	4884	1315954	1315325	630						
1385	4885	1316338	1317444	1107	sp CCPA_BACME	Bacillus megaterium ccpA	31.4	31.4	328	glucose-resistance amylase regulator (catabolite control protein)
1386	4886	1317434	1319005	1572	sp RBSA_ECOLI	Escherichia coli K12 rbsA	44.7	76.2	499	ribose transport ATP-binding protein
1387	4887	1319005	1319976	972	sp RBSC_ECOLI	Escherichia coli K12 MG1655 rbsC	45.6	76.9	329	high affinity ribose transport protein
1388	4888	1320001	1320942	942	sp RBSB_ECOLI	Escherichia coli K12 MG1655 rbsB	45.9	77.7	305	periplasmic ribose-binding protein
1389	4889	1320952	1321320	369	sp RBSD_ECOLI	Escherichia coli K12 MG1655 rbsD	41.7	68.4	139	high affinity ribose transport protein
1390	4890	1321476	1322111	636	sp YIW2_YEAST	Saccharomyces cerevisiae YIR042c	31.0	58.0	200	hypothetical protein
1391	4891	1322393	1323406	1014	gp SCF34_13	Streptomyces coelicolor SCF34.13c	31.4	60.2	354	iron-siderophore binding lipoprotein
1392	4892	1323533	1324537	1005	sp NTCI_RAT	Rattus norvegicus (Rat) NTCI	35.8	61.9	268	Na-dependent bile acid transporter
1393	4893	1324778	1326256	1479	gsp W61457	Staphylococcus aureus WHO 29 ratB	43.1	71.8	485	RNA-dependent amidotransferase B
1394	4894	1326378	1327049	672	sp F4RE_METJA	Methanococcus jannaschii MJ1501 f4re	32.6	61.1	172	putative F420-dependent NADH reductase
1395	4895	1330967	1329891	1077	sp YQJG_ECOLI	Escherichia coli K12 yqjG	39.8	66.9	317	hypothetical protein
1396	4896	1331102	1331875	774	pir A70672	Mycobacterium tuberculosis H37Rv Rv2972c	39.3	62.4	234	hypothetical protein
1397	4897	1331953	1333008	1056	pir H70855	Mycobacterium tuberculosis H37Rv Rv3005c	27.4	52.6	325	hypothetical membrane protein
1398	4898	1333424	1333188	237						
1399	4899	1335280	1333442	1839	gp AJ012293_1	Corynebacterium glutamicum ATCC 13032 ilvD	99.2	99.4	613	dihydroxy-acid dehydratase
1400	4900	1335975	1335412	564	pir G70855	Mycobacterium tuberculosis H37Rv Rv3004	33.3	68.6	105	hypothetical protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1401	4901	1337567	1336095	1473	sp YILV_CORGL	Corynebacterium glutamicum ATCC 13032 yilV	100 0	100 0	62	hypothetical membrane protein
1402	4902	1338639	1338379	231	GP SSU18930_26 3	Sulfolobus solfataricus	45 0	55 0	66	hypothetical protein
1403	4903	1342072	1342677	606						
1404	4904	1342457	1341960	498	sp NRTD_SYNP7	Synechococcus sp nrtD	50.9	80 8	167	nitrate transport ATP-binding potein
1405	4905	1342727	1342461	267	sp MALK_ENTAE	Enterobacter aerogenes (Aerobacter aerogenes) malK	46.0	78 2	87	maltose/maltodextrin transport ATP-binding protein
1406	4906	1343675	1342794	882	sp NRTA_ANASP	Anabaena sp strain PCC 7120 nrtA	28 1	56 8	324	nitrate transporter protein
1407	4907	1344018	1344464	447						
1408	4908	1344440	1344808	369						
1409	4909	1344935	1345420	486	sp DIM6_STRCO	Streptomyces coelicolor	39.4	73 2	142	actinorhodin polyketide dimerase
1410	4910	1345486	1346439	954	sp CZCD_ALCEU	Ralstonia eutropha czcD	39 1	72 7	304	cobalt-zinc-cadimium resistance protein
1411	4911	1345487	1345335	153						
1412	4912	1346331	1345642	690						
1413	4913	1346458	1348272	1815	sp Y666_METJA	Methanococcus jannaschii	22 9	53 7	642	hypothetical protein
1414	4914	1348334	1350076	1743						
1415	4915	1350855	1352444	1590	gsp Y22646	Brevibacterium flavum serA	99.8	100 0	530	D 3-phosphoglycerate dehydrogenase
1416	4916	1352053	1351727	327	SP YEN1_SCHPO	Sch zosaccharomyces pombe SPAC11G7 01	29 0	52 0	105	hypothetical serine-rich protein
1417	4917	1352585	1353451	867						
1418	4918	1355601	1354540	1062						
1419	4919	1355689	1357554	1866	pir T03476	Rhodobacter capsulatus strain SB1003	32 9	63 1	620	hypothetical protein
1420	4920	1356452	1356853	402						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1421	4921	1357557	1358210	654						
1422	4922	1358259	1359062	804	sp HPCE_ECOLI	Escherichia coli C hpcE	33 3	59 2	228	homoprotocatechiuate catabolism bifunctional isomerase/decarboxylase [includes 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase(hhdd isomerase), 5-carboxymethyl-2-oxo-hex-3-ene-1,7-dioate decarboxylase(opet decarboxylase)]
1423	4923	1359053	1359669	618	sp UBIG_ECOLI	Escherichia coli K12	23 4	55.7	192	methyltransferase or 3-demethylubiquinone-9 3-O-methyltransferase
1424	4924	1361295	1360168	1128	sp DHBC_BACSU	Bacillus subtilis dhbC	38.0	70 4	371	isochorismate synthase
1425	4925	1361361	1362848	1488	sp SYE_BACSU	Bacillus subtilis gltX	37 3	69 7	485	glutamyl-tRNA synthetase
1426	4926	1363138	1362926	213	gp SCJ33_10	Streptomyces coelicolor A3(2)	77 0	90 0	67	transcriptional regulator
1427	4927	1363657	1363142	516						
1428	4928	1364253	1363732	522						
1429	4929	1364915	1365256	342						
1430	4930	1364960	1364340	621						
1431	4931	1365180	1364878	303						
1432	4932	1365396	1365217	180						
1433	4933	1365808	1366137	330						
1434	4934	1367293	1367505	213						
1435	4935	1368070	1367888	183						
1436	4936	1368078	1368395	318						
1437	4937	1368400	1369551	1152						
1438	4938	1369551	1369874	324						
1439	4939	1371637	1369877	1761	sp THIC_BACSU	Bacillus subtilis thiA or thiC	65 1	81.0	599	thiamin biosynthesis protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Termina (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarty (%)	Matched length (a a)	Function
1440	4940	1372326	1371979	348						
1441	4941	1372601	1373131	531						
1442	4942	1373798	1373929	132	GSP Y37857	Chlamydia trachomatis	61.0	74.0	44	lipoprotein
1443	4943	1374556	1375491	936						
1444	4944	1375776	1373350	2427	sp PHS1_RAT	Rattus norvegicus (Rat)	44.2	74.0	797	glycogen phosphorylase
1445	4945	1375987	1375805	183						
1446	4946	1376088	1375933	156						
1447	4947	1377555	1376149	1407	sp YRKH_BACSU	Bacillus subtilis yrkH	25.4	52.8	299	hypothetical protein
1448	4948	1378415	1377666	750	sp Y441_METJA	Methanococcus jannaschii Y441	25.4	64.8	256	hypothetical membrane protein
1449	4949	1378942	1378466	477						
1450	4950	1379003	1379566	564	sp SPOT_ECOLI	Escherichia coli K12 spoT	29.8	60.1	178	guanosine 3',5'-bis(diphosphate) 3'-pyrophosphatase
1451	4951	1380259	1379555	705	sp ICLR_ECOLI	Escherichia coli K12 iclR	26.1	60.7	257	acetate repressor protein
1452	4952	1380440	1381882	1443	sp LEU2_ACTTI	Actinoplanes teichomyceticus leu2	68.1	87.5	473	3-isopropylmalate dehydratase large subunit
1453	4953	1381902	1382492	591	sp LEUD_SALTY	Salmonella typhimurium	67.7	89.2	195	3-isopropylmalate dehydratase small subunit
1454	4954	1382819	1382502	318						
1455	4955	1383798	1382845	954	gp MLCB637_35	Mycobacterium tuberculosis H37Rv MLCB637.35c	45.9	71.4	294	mutator mutT protein ((7,8-dihydro 8-oxoguanine-triphosphatase)(8-oxo-dGTPase)(dGTP pyrophosphohydrolase)
1456	4956	1383930	1384085	156						
1457	4957	1384130	1385125	996	sp GPDA_BACSU	Bacillus subtilis gpdA	45.0	72.2	331	NAD(P)H-dependent dihydroxyacetone phosphate reductase
1458	4958	1385153	1386232	1080	sp DDLA_ECOLI	Escherichia coli K12 MG1655 ddlA	40.4	67.4	374	D-alanine D-alanine ligase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (aa)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (aa)	Function
1459	4959	1387270	1386293	978						
1460	4960	1387332	1388324	993	sp THIL_ECOLI	Escherichia coli K12 thiL	32.2	57.6	335	thiamin-phosphate kinase
1461	4961	1388312	1389073	762	sp UNG_MOUSE	Mus musculus ung	38.8	59.6	245	uracil-DNA glycosylase precursor
1462	4962	1389208	1390788	1581	sp Y369_MYCGE	Mycoplasma genitalium (SGC3) MG369	23.1	56.3	568	hypothetical protein
1463	4963	1390796	1392916	2121	sp RECG_ECOLI	Escherichia coli K12 recG	35.4	60.0	693	ATP-dependent DNA helicase
1464	4964	1391961	1391638	324	GSP Y75303	Neisseria meningitidis	31.0	48.0	108	polypeptides predicted to be useful antigens for vaccines and diagnostics
1465	4965	1392930	1393151	213	sp BCCP_PROFR	Propionibacterium freudenreichii subsp. Shermanii	38.8	67.2	67	biotin carboxyl carrier protein
1466	4966	1393154	1393735	582	sp YHHF_ECOLI	Escherichia coli K12 yhhF	37.1	63.5	167	methylase
1467	4967	1393742	1394221	480	sp KDTB_ECOLI	Escherichia coli K12 MG1655 kdtB	42.6	78.7	155	lipopolysaccharide core biosynthesis protein
1468	4968	1394854	1395933	1080						
1469	4969	1394894	1395097	204	GSP Y75358	Neisseria gonorrhoeae	67.0	74.0	65	Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics
1470	4970	1395549	1394800	750	sp GLNQ_BACST	Bacillus stearothermophilus glnQ	56.4	78.6	252	ABC transporter or glutamine ABC transporter, ATP-binding protein
1471	4971	1396410	1395568	843	sp NOCM_AGRT5	Agrobacterium tumefaciens nocM	32.7	75.0	220	nopaline transport protein
1472	4972	1397421	1396561	861	sp GLNH_ECOLI	Escherichia coli K12 MG1655 glnH	27.4	59.0	234	glutamine-binding protein precursor
1473	4973	1397662	1398468	807						
1474	4974	1399534	1398557	978	pir H69160	Methanobacterium thermoautotrophicum MTH465	28.6	60.3	322	hypothetical membrane protein
1475	4975	1400926	1401333	408						
1476	4976	1400947	1400185	750	sp VINT_BPL54	Bacteriophage L54a vinT	26.9	52.5	223	phage integrase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1477	4977	1401333	1402076	744						
1478	4978	1402272	1402703	432						
1479	4979	1402874	1402368	507						
1480	4980	1403128	1403991	864						
1481	4981	1403997	1404215	219						
1482	4982	1404885	1404694	192	pir S60890	Corynebacterium glutamicum orf2	88.5	96.2	26	insertion element (IS3 related)
1483	4983	1406174	1405320	855						
1484	4984	1407109	1406999	111	PIR S60890	Corynebacterium glutamicum	89.0	97.0	37	hypothetical protein
1485	4985	1407535	1407167	369						
1486	4986	1407873	1407559	315						
1487	4987	1409023	1408703	321						
1488	4988	1409802	1409428	375						
1489	4989	1411011	1410064	948						
1490	4990	1411424	1411119	306						
1491	4991	1412000	1411437	564						
1492	4992	1412351	1412572	222						
1493	4993	1412916	1412626	291						
1494	4994	1413745	1416459	2715	sp DPO1_MYCTU	Mycobacterium tuberculosis polA	56.3	80.8	896	DNA polymerase I
1495	4995	1417883	1416462	1422	sp CMCT_NOCLA	Streptomyces lactamdurans cmcT	33.8	67.8	456	cephamycin export protein
1496	4996	1417962	1418870	909	gp SCJ9A_15	Streptomyces coelicolor A3(2) SCJ9A.15c	41.3	65.4	283	DNA-binding protein
1497	4997	1418876	1419748	873	sp MORA_PSEPU	Pseudomonas putida morA	46.5	76.1	284	morphine 6-dehydrogenase
1498	4998	1420036	1419878	159						

Table 1 (continued)

SEQ NO DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1499	4999	1420724	1420071	654	sp YAFE_ECOLI	Streptomyces coelicolor SCH5 13 yafE	31.9	58 3	163	hypothetical protein
1500	5000	1421099	1422556	1458	sp RS1_ECOLI	Escherichia coli K12 rpsA	39.5	71 4	451	30S ribosomal protein S1
1501	5001	1422571	1421096	1476						
1502	5002	1425279	1425878	600	sp YACE_BRELA	Brevibacterium lactofermentum ATCC 13869 yacE	80.5	93 9	195	hypothetical protein
1503	5003	1426257	1427354	1098						
1504	5004	1427957	1427376	582						
1505	5005	1428049	1427804	246						
1506	5006	1428290	1429246	957						
1507	5007	1429159	1429224	936	sp IUNH_CRIFA	Crithidia fasciculata iunH	61 9	81 0	310	inosine-uridine preferring nucleoside hypolase (purine nucleosidase)
1508	5008	1430642	1429194	1449	sp QACA_STAAU	Staphylococcus aureus	23 6	53 8	517	aniseptic resistance protein
1509	5009	1431579	1430659	921	sp RBSK_ECOLI	Escherichia coli K12 rbsK	35 5	67.6	293	ribose kinase
1510	5010	1432612	1431575	1038	sp ASCG_ECOLI	Escherichia coli K12 ascG	30 0	65.6	337	criptic asc operon repressor, ranscription regulator
1511	5011	1432750	1433547	798						
1512	5012	1434105	1436201	2097	sp UVRB_STRPN	Streptococcus pneumoniae plasmid pSB470 uvrB	57.4	83 3	671	excinuclease ABC subunit B
1513	5013	1436335	1436775	441	sp Y531_METJA	Methanococcus jannaschii MJ0531	33 6	59 2	152	hypothetical protein
1514	5014	1437249	1436969	381	sp YTFH_ECOLI	Escherichia coli K12 ytfH	38 8	80 2	121	hypothetical protein
1515	5015	1437356	1438201	846	sp YTFG_ECOLI	Escherichia coli K12 ytfG	53 8	77 1	279	hypothetical protein
1516	5016	1439343	1440026	684						
1517	5017	1440560	1438212	2349	pir H70040	Bacillus subtilis yvgS	23 2	47.2	839	hypothetical protein
1518	5018	1441586	1440675	912	gp SC9H11_26	Streptomyces coelicolor A3(2) SC9H11.26c	32 7	68 0	150	hypothetical protein
1519	5019	1442392	1441793	600	sp YCBL_ECOLI	Escherichia coli K12 ycbL	30 4	58 4	214	hydrolase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
1520	5020	1442487	1445333	2847	sp UVRA_ECOLI	Escherichia coli K12 uvrA	56.2	80.6	952	excinuclease ABC subunit A
1521	5021	1444115	1443810	306	PIR JQ0406	Micrococcus luteus	40.0	57.0	100	hypothetical protein 1246 (uvrA region)
1522	5022	1445393	1444944	450	PIR JQ0406	Micrococcus luteus	31.0	47.0	142	hypothetical protein 1246 (uvrA region)
1523	5023	1446158	1446874	717						
1524	5024	1447446	1445323	2124						
1525	5025	1447792	1448358	567	sp IF3_RHOSH	Rhodobacter sphaeroides infC	52.5	78.2	179	translation initiation factor IF-3
1526	5026	1448390	1448581	192	sp RL35_MYCFE	Mycoplasma fermentans	41.7	76.7	60	50S ribosomal protein L35
1527	5027	1448645	1449025	381	sp RL20_PSESY	Pseudomonas syringae pv syringae	75.0	92.7	117	50S ribosomal protein L20
1528	5028	1449940	1449119	822						
1529	5029	1450125	1450692	567						
1530	5030	1450918	1451820	903	sp UGPA_ECOLI	Escherichia coli K12 MG1655 ugpA	33.2	71.6	292	sn-glycerol-3-phosphate transport system permease protein
1531	5031	1451820	1452653	834	sp UGPE_ECOLI	Escherichia coli K12 MG1655 ugpE	33.3	70.4	270	sn-glycerol-3-phosphate transport system protein
1532	5032	1452758	1454071	1314	sp UGPB_ECOLI	Escherichia coli K12 MG1655 ugpB	26.6	57.6	436	sn-glycerol-3-phosphate transport system permease proein
1533	5033	1454115	1455338	1224	sp UGPC_ECOLI	Escherichia coli K12 MG1655 ugpC	44.0	71.3	393	sn-glycerol-3-phosphate transport ATP binding protein
1534	5034	1454350	1454102	249	PIR F72756	Aeropyrum pernix K1 APE0042	47.0	56.0	74	hypothetical protein
1535	5035	1456036	1455350	717	sp GLPQ_BACSU	Bacillus subtilis glpQ	26.2	50.0	244	glycerophosphoryl diester phosphodiesterase
1536	5036	1456355	1456948	594	sp TRMH_ECOLI	Escherichia coli K12 MG1655 trmH	34.0	71.2	153	tRNA(guanosine-2'-O-)-methlytransferase
1537	5037	1457047	1458066	1020	sp SYFA_BACSU	Bacillus subtilis 168 syfA				phenylalanyl tRNA synthetase alpha chain

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
1538	5038	1458133	1460616	2484	sp SYFB_ECOLI	Escherichia coli K12 MG1655 syfB	42.6	71.7	343	phenylalanyl-tRNA synthetase beta chain
1539	5039	1458966	1458196	771						
1540	5040	1461157	1462128	972	sp ESTA_STRSC	Streptomyces scabies estA	26.5	55.1	363	esterase
1541	5041	1462134	1463516	1383	sp MDMB_STRMY	Streptomyces mycarofaciens mdmB	30.0	56.3	423	macrolide 3-O-acyltransferase
1542	5042	1463533	1463934	402						
1543	5043	1464083	1465123	1041	gp AF005242_1	Corynebacterium glutamicum ASO19 argC	98.3	99.1	347	N-acetylglutamate-5-semialdehyde dehydrogenase
1544	5044	1465210	1466373	1164	sp ARGJ_CORGL	Corynebacterium glutamicum ATCC 13032 argJ	99.5	99.7	388	glutamate N-acetyltransferase
1545	5045	1467376	1468548	1173	sp ARGD_CORGL	Corynebacterium glutamicum ATCC 13032 argD	99.0	99.2	391	acetylornithine aminotransferase
1546	5046	1470211	1471413	1203	sp ASSY_CORGL	Corynebacterium glutamicum ASO19 argG	99.5	99.5	401	argininosuccinate synthetase
1547	5047	1471362	1470154	1209						
1548	5048	1471477	1472907	1431	gp AF048764_1	Corynebacterium glutamicum ASO19 argH	83.3	90.0	478	argininosuccinate lyase
1549	5049	1472977	1474119	1143						
1550	5050	1474119	1475693	1575						
1551	5051	1475683	1476294	612						
1552	5052	1476343	1476519	177	sp YCAR_ECOLI	Escherichia coli K12 ycaR	48.0	72.0	50	hypothetical protein
1553	5053	1476550	1477809	1260	sp SYY1_BACSU	Bacillus subtilis syy1	48.4	79.6	417	tyrosyl-tRNA synthase (tyrosine--tRNA ligase)
1554	5054	1478393	1477929	465	sp Y531_METJA	Methanococcus jannaschii MJ0531	26.9	64.4	149	hypothetical protein
1555	5055	1478692	1478503	390						
1556	5056	1483475	1483335	141	PIR F81737	Chlamydia muridarum Nigg TC0129	71.0	75.0	42	hypothetical protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1557	5057	1483936	1483724	273	GSP:Y35814	Chlamydia pneumoniae	61.0	66.0	84	hypothetical protein
1558	5058	1484675	1486027	1353	sp:IF2_BORBU	Borrelia burgdorferi IF2	36.3	67.0	182	translation initiation factor IF-2
1559	5059	1486042	1487025	984	sp:YZGD_BACSU	Bacillus subtilis yzgD	29.6	60.1	311	hypothetical protein
1560	5060	1487032	1487193	162						
1561	5061	1487238	1488056	819	sp:YQXC_BACSU	Bacillus subtilis yqxC	38.5	69.6	260	hypothetical protein
1562	5062	1488146	1489018	873	sp:YEJB_HAEIN	Mycobacterium tuberculosis H37Rv Rv1695	31.6	31.6	225	hypothetical protein
1563	5063	1489103	1490881	1779	sp:RECN_ECOLI	Escherichia coli K12 recN	31.4	63.4	574	DNA repair protein
1564	5064	1490944	1492134	1191	pir:H70502	Mycobacterium tuberculosis H37Rv Rv1697	41.9	73.1	394	hypothetical protein
1565	5065	1492147	1493109	963	pir:A70503	Mycobacterium tuberculosis H37Rv Rv1698	30.4	68.1	313	hypothetical protein
1566	5066	1493513	1495174	1662	sp:PYRG_ECOLI	Escherichia coli K12 pyrG	55.0	76.7	549	CTP synthase (UTP--ammonia ligase)
1567	5067	1495205	1495861	657	sp:YQKG_BACSU	Bacillus subtilis yqkG	36.3	71.3	157	hypothetical protein
1568	5068	1495861	1496772	912	gp:AF093548_1	Staphylococcus aureus xerD	39.7	71.7	300	tyrosine recombinase
1569	5069	1496324	1496795	1530	sp:TLRC_STRFR	Streptomyces fradiae tlrC	30.5	59.7	551	tylosin resistance ATP-binding protein
1570	5070	1498863	1499645	783	gp:CCU87804_4	Caulobacter crescentus parA	44.6	73.6	258	chromosome partitioning protein or ATPase involved in active partitioning of diverse bacterial plasmids
1571	5071	1499931	1500695	765	sp:YPUG_BACSU	Bacillus subtilis ypuG	28.3	64.5	251	hypothetical protein
1572	5072	1501471	1500911	561						
1573	5073	1501710	1502576	867	gp:AF109155_1	Datisca glomerata tst	35.6	67.0	270	thiosulfate sulfurtransferase
1574	5074	1502634	1503176	543	sp:YPUH_BACSU	Bacillus subtilis ypuH	33.1	65.7	172	hypothetical protein
1575	5075	1503483	1504238	756	sp:RLUB_BACSU	Bacillus subtilis rluB	45.9	72.5	229	ribosomal large subunit pseudouridine synthase B

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
1576	5076	1504256	1504945	690	sp KCY_BACSU	Bacillus subtilis cmk	38.6	73.6	220	cytidylate kinase
1577	5077	1505017	1506573	1557	sp YPHC_BACSU	Bacillus subtilis yphC	42.8	74.0	435	GTP binding protein
1578	5078	1507327	1506662	666						
1579	5079	1507902	1507405	498						
1580	5080	1508729	1507917	813	sp YY42_MYCTU	Mycobacterium tuberculosis Rv3342	36.2	67.2	232	methyltransferase
1581	5081	1508813	1510366	1554	prf 2513302B	Corynebacterium striatum M82B tetA	29.7	60.1	499	ABC transporter
1582	5082	1510366	1512132	1767	prf 2513302A	Corynebacterium striatum M82B tetB	31.2	56.3	602	ABC transporter
1583	5083	1511667	1510843	825						
1584	5084	1512189	1512977	789	sp YGIE_ECOLI	Escherichia coli K12 ygiE	39.7	73.2	257	hypothetical membrane protein
1585	5085	1514505	1514693	189						
1586	5086	1514527	1512980	1548	gp AB029555_1	Bacillus subtilis ATCC 9372 nhaG	25.7	61.5	499	Na+/H+ antiporter
1587	5087	1515159	1514974	186						
1588	5088	1515396	1515815	420						
1589	5089	1515782	1515408	375	sp YCHJ_ECOLI	Escherichia coli K12 o249#9 ychJ	36.9	57.7	130	hypothetical protein
1590	5090	1516962	1515799	1164	pir C69334	Archaeoglobus fulgidus AF0675	25.2	63.8	210	2-hydroxy 6-oxohepta-2,4-dienoate hydrolase
1591	5091	1517170	1519458	2289	sp SECA_BACSU	Bacillus subtilis secA	35.2	61.7	805	preprotein translocase SecA subunit
1592	5092	1519601	1520029	429	gp AF173844_2	Mycobacterium smegmatis garA	75.8	93.2	132	signal transduction protein
1593	5093	1520190	1520945	756	sp Y0DF_MYCTU	Mycobacterium tuberculosis H37Rv Rv1828	41.9	74.4	234	hypothetical protein
1594	5094	1520957	1521589	633	sp Y0DE_MYCTU	Mycobacterium tuberculosis H37Rv Rv1828	30.8	63.2	133	hypothetical protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Termina (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1595	5095	1521771	1522343	573	sp Y0DE_MYCTU	Mycobacterium tuberculosis H37Rv Rv1828	71 4	84 3	178	hypothetical protein
1596	5096	1522041	1522432	510						
1597	5097	1524500	1523052	1449						
1598	5098	1525374	1525973	600						
1599	5099	1525497	1524568	930						
1600	5100	1526534	1525473	1062	sp YHDP_BACSU	Bacillus subtilis yhdP	33 9	69 0	342	hemolysin
1601	5101	1527913	1526534	1380	sp YHDT_BACSU	Bacillus subtilis yhdT	31 4	65 5	65	hemolysin
1602	5102	1527969	1528186	219						
1603	5103	1529330	1527987	1344	gp TTHERAGEN_1	Thermus thermophilus herA	41 2	69 5	374	DEAD box RNA helicase
1604	5104	1529486	1530220	735	sp YD48_MYCTU	Mycobacterium tuberculosis H37Rv Rv1348	34 3	66 1	245	ABC transporter ATP-binding protein
1605	5105	1531816	1530341	1476	gsp W27613	Brevibacterium flavum	99 0	99 2	492	6-phosphogluconate dehydrogenase
1606	5106	1531933	1532394	462	pir G70664	Mycobacterium tuberculosis H37Rv Rv1847	39 7	67 8	121	thioesterase
1607	5107	1532322	1532996	675						
1608	5108	1533041	1533781	741	sp NODI_RHIS3	Rhizobium sp. N33 nodI	39 6	68 1	235	nodulation ATP binding protein I
1609	5109	1533781	1534521	741	pir E70501	Mycobacterium tuberculosis H37Rv Rv1686c	43 1	76 3	232	hypothetical membrane protein
1610	5110	1535401	1534529	873	sp YFHH_ECOLI	Escherichia coli K12 yfhH	26 7	63 9	277	transcriptional regulator
1611	5111	1536227	1535382	846	sp PHNE_ECOLI	Escherichia coli K12 phnE	29 9	63 4	281	phosphonates transport system permease protein
1612	5112	1537030	1536227	804	sp PHNE_ECOLI	Escherichia coli K12 phnE	27 2	62 3	268	phosphonates transport system permease protein
1613	5113	1537833	1537030	804	sp PHNC_ECOLI	Escherichia coli K12 phnC	44 8	72 0	250	phosphonates transport ATP-binding protein
1614	5114	1538759	1538968	210						
1615	5115	1538919	1537870	1050						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1616	5116	1539664	1538963	702						
1617	5117	1541403	1539820	1584	sp THID_SALTY	Salmonella typhimurium thiD	47.3	70.2	262	phosphomethylpyrimidine kinase
1618	5118	1542922	1542119	804	sp THIM_SALTY	Salmonella typhimurium LT2 thiM	46.6	77.5	249	hydoxyethylthiazole kinase
1619	5119	1544976	1546289	1314	pir I70830	Mycobacterium tuberculosis H37Rv ufaA1	28.6	55.0	451	cyclopropane-fatty-acyl-phospholipid synthase
1620	5120	1547692	1546307	1386	prf 2223339B	Burkholderia cepacia Pc701 mopB	32.5	66.9	468	sugar transporter or 4-methyl-o-phthalate/phthalate permease
1621	5121	1548440	1547967	474	prf 2120352B	Thermus flavus AT-62 gpt	36.5	59.0	156	purine phosphoribosyltransferase
1622	5122	1548651	1549349	699	sp YEBN_ECOLI	Escherichia coli K12 yebN	39.8	68.5	206	hypothetical protein
1623	5123	1549403	1550398	996	gp AF178758_2	Sinorhizobium sp. As4 arsB	23.3	54.6	361	arsenic oxyanion-translocation pump membrane subunit
1624	5124	1550469	1550951	483						
1625	5125	1551545	1552237	693	gp SCI7_33	Streptomyces coelicolor A3(2) SCI7.33	62.2	83.8	222	hypothetical protein
1626	5126	1552518	1553972	1455	gp PSTRTETC1_6	Pseudomonas sp. R9 ORFA	51.8	83.6	469	sulfate permease
1627	5127	1553722	1553297	426	GP PSTRTETC1_7	Pseudomonas sp. R9 ORFG	39.0	50.0	97	hypothetical protein
1628	5128	1554684	1554070	615						
1629	5129	1554861	1555067	207						
1630	5130	1555079	1554891	189						
1631	5131	1555835	1555086	750						
1632	5132	1556376	1556771	396	pir A70945	Mycobacterium tuberculosis H37Rv Rv2050	71.8	87.3	110	hypothetical protein
1633	5133	1557823	1557014	810	prf 2317468A	Schizosaccharomyces pombe dpm1	39.2	71.0	217	dolichol phosphate mannose synthase
1634	5134	1559493	1557859	1635	sp LNT_ECOLI	Escherichia coli K12 lnt	25.1	55.6	527	apolipoprotein N-acyltransferase
1635	5135	1560237	1559497	741						
1636	5136	1561660	1560437	1224	gp AF188894_1	Candida albicans lip1	23.7	55.6	392	secretory lipase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
1637	5137	1561780	1562553	774	pir C70764	Mycobacterium tuberculosis H37Rv cobG	31.3	56.7	291	precorrin 2 methyltransferase
1638	5138	1563802	1562525	1278	sp COBL_PSEDE	Pseudomonas denitrificans SC510 cobL	32.4	60.8	411	precorrin 6Y C5, 15 methyltransferase
1639	5139	1563872	1564237	366						
1640	5140	1564237	1564482	246						
1641	5141	1565362	1564569	738	sp YY12_MYCTU	Mycobacterium tuberculosis H37Rv Rv3412	54.1	75.4	244	oxidoreductase
1642	5142	1566438	1565302	1137	gp AF014460_1	Streptococcus mutans LT11 pepQ	30.1	61.3	382	dipeptidase or X-Pro dipeptidase
1643	5143	1566468	1567106	639						
1644	5144	1569903	1567117	2787	sp MTR4_YEAST	Saccharomyces cerevisiae YJL050W dob1	26.5	55.7	1030	ATP-dependent RNA helicase
1645	5145	1570933	1569932	1002	sp TATC_ECOLI	Escherichia coli K12 tatC	28.7	62.7	268	sec-independent protein translocase protein
1646	5146	1571382	1571068	315	sp YY34_MYCLE	Mycobacterium leprae MLCB2533.27	44.7	69.4	85	hypothetical protein
1647	5147	1572486	1571506	981	sp YY35_MYCTU	Mycobacterium tuberculosis H37Rv Rv2095c	31.9	61.2	317	hypothetical protein
1648	5148	1573463	1572492	972	sp YY36_MYCLE	Mycobacterium leprae MLCB2533.25	32.4	64.8	324	hypothetical protein
1649	5149	1574915	1573491	1425	sp YY37_MYCTU	Mycobacterium tuberculosis H37Rv Rv2097c	53.1	77.3	467	hypothetical protein
1650	5150	1574957	1575205	249						
1651	5151	1575136	1574945	192	pir B70512	Mycobacterium tuberculosis H37Rv Rv2111c	54.1	80.3	61	hypothetical protein
1652	5152	1576947	1575406	1542	pir C70512	Mycobacterium tuberculosis H37Rv Rv2112c	48.6	74.2	516	hypothetical protein
1653	5153	1577327	1577808	480	PIR H72504	Aeropyrum pernix K1 APE2014	42.0	50.0	159	hypothetical protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1654	5154	1578531	1576951	1581	prf 2422382Q	Rhodococcus erythropolis arc	51.6	78.5	545	AAA family ATPase (chaperone-like function)
1655	5155	1579400	1578567	834	pir S72844	Mycobacterium leprae pimT	57.3	79.0	281	protein-beta-aspartate methyltransferase
1656	5156	1580771	1579449	1323	gp AF005050_1	Homo sapiens	38.1	67.2	436	aspartyl aminopeptidase
1657	5157	1580807	1581640	834	pir B70513	Mycobacterium tuberculosis H37Rv Rv2119	45.4	71.4	269	hypothetical protein
1658	5158	1581851	1582114	264	sp VAPI_BACNO	Dichelobacter nodosus A198 vapI	40.6	72.5	69	virulence associated protein
1659	5159	1583481	1582273	1209	prf 2513209A	Staphylococcus aureus norA23	21.8	61.0	385	quinolon resistance protein
1660	5160	1585490	1583913	1578	sp ASPA_CORGL	Corynebacterium glutamicum (Brevibacterium flavum) MJ233 aspA	99.8	99.8	526	aspartate ammonia-lyase
1661	5161	1586445	1585603	843	gp AF050166_1	Corynebacterium glutamicum ASO19 hisG	96.8	97.5	281	ATP phosphor bosyltransferase
1662	5162	1587504	1586812	693	pir H72277	Thermotoga maritima MSB8 TM1254	30.8	63.1	195	beta-phosphoglucomutase
1663	5163	1591235	1587573	3663	sp METH_ECOLI	Escherichia coli K12 metH	31.6	62.4	1254	5-methyltetrahydrofolate--homocysteine methyltransferase
1664	5164	1591343	1591912	570						
1665	5165	1592366	1591041	1026	sp AHPF_XANCH	Xanthomonas campestris ahpF	22.4	49.5	366	alkyl hydroperoxide reductase subunit F
1666	5166	1593337	1594512	1176	sp ACR3_YEAST	Saccharomyces cerevisiae S288C YPR201W acr3	33.0	63.9	388	arsenical-resistance protein
1667	5167	1594532	1594951	420	sp ARSC_STAAU	Staphylococcus aureus plasmid pI258 arsC	32.6	64.3	129	arsenate reductase
1668	5168	1595030	1595668	639	pir G70964	Mycobacterium tuberculosis H37Rv arsC	47.2	75.6	123	arsenate reductase
1669	5169	1596221	1595844	378						
1670	5170	1597460	1596249	1212	sp SYC_ECOLI	Escherichia coli K12 cysS	35.9	64.3	387	cysteinyl-tRNA synthetase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	nitial (nt)	Terminal (nt)	ORF (bp)	db Match	Homolngous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1671	5171	1598623	1597745	879	sp BACA_ECOLI	Escherichia coli K12 bacA	37.3	69.4	255	bacitracin resistance protein
1672	5172	1598607	1599614	948	prf 2214302F	Agrobacterium tumefaciens mocA	33.4	62.6	326	oxidoreductase
1673	5173	1599679	1600677	999	pir F70577	Mycobacterium tuberculosis H37Rv lppI.	27.0	53.5	359	lipoprotein
1674	5174	1600692	1601804	1113	sp PYRD_AGRAE	Agrocybe aegerita ura1	44.0	67.1	334	dihydroorotate dehydrogenase
1675	5175	1602281	1601931	351						
1676	5176	1602660	1603466	807						
1677	5177	1603520	1604629	1110	gp PSESTBCBAD_1	Pseudomonas syringae tnpA	34.7	55.3	360	transposase
1678	5178	1605315	1604830	486						
1679	5179	1605811	1605281	531	sp YBHB_ECOLI	Escherichia coli K12 ybhB	44.1	75.0	152	bio operon ORF I (biotin biosynthetic enzyme)
1680	5180	1605961	1606689	729	GSP Y74829	Neisseria meningitidis	26.0	33.0	198	Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics
1681	5181	1607645	1608248	603						
1682	5182	1607657	1605861	1797	prf 2513302A	Corynebacterium striatum M82B tetB	43.6	68.7	597	ABC transporter
1683	5183	1609087	1609335	249						
1684	5184	1609247	1607661	1587	prf 2513302B	Corynebacterium striatum M82B tetA	36.8	67.1	535	ABC transporter
1685	5185	1610192	1609842	351						
1686	5186	1610236	1610844	609	pir JU0052	Streptomyces anulatus pac	32.4	56.4	56	puromycin N-acetyltransferase
1687	5187	1612238	1611150	1089	sp ARGK_ECOLI	Escherichia coli K12 argK	43.1	72.3	339	LAO(lysine, arginine, and ornithine)/AO (arginine and ornithine)transport system kinase
1688	5188	1614444	1612234	2211	sp MUTB_STRCM	Streptomyces cinnamonensis A3823.5 mutB	72.2	87.5	741	methylmalonyl-CoA mutase alpha subunit

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1689	5189	1616298	1614451	1848	sp MUTA_STRCM	Streptomyces cinnamonensis A3823 5 mutA	41.6	68 2	610	methylmalonyl-CoA mutase beta subunit
1690	5190	1616578	1617300	723	sp YS13_MYCTU	Mycobacterium tuberculosis H37Rv Rv1491c	39.7	70 1	224	hypothetical membrane protein
1691	5191	1617398	1617994	597						
1692	5192	1619616	1618321	1296	sp YS09_MYCTU	Mycobacterium tuberculosis H37Rv Rv1488	64.1	87.0	370	hypothetical membrane protein
1693	5193	1620106	1619672	435	p r B70711	Mycobacterium tuberculosis H37Rv Rv1487	44 7	78 7	141	hypothetical membrane protein
1694	5194	1621009	1620167	843	gp SCC77_24	Streptomyces coelicolor A3(2) SCC77 24	51 0	72 8	261	hypothetical protein
1695	5195	1621056	1621838	783						
1696	5196	1622950	1621841	1110	sp HEMZ_PROFR	Propionibacterium freudenreichii subsp. Shermanii hemH	36 8	65 7	364	ferrochelatase
1697	5197	1624826	1623027	1800	sp P54_ENTFC	Streptococcus faecium	25.5	56 5	611	invasin
1698	5198	1625925	1625428	498						
1699	5199	1626279	1629107	2829	pir F70873	Mycobacterium tuberculosis H37Rv acn	69.9	85.9	959	aconitate hydratase
1700	5200	1629298	1629861	564	pir E70873	Mycobacterium tuberculosis H37Rv Rv1474c	54.6	81 6	174	transcriptional regulator
1701	5201	1629913	1630668	756	pir F64496	Methanococcus jannaschii MJ1575 guaA	21.3	51.9	235	GMP synthetase
1702	5202	1631329	1630667	663	gp SCD82_4	Streptomyces coelicolor A3(2) SCD82 04c	32.6	62.0	221	hypothetical protein
1703	5203	1631660	1631926	267	pir E64494	Methanococcus jannaschii MJ1558	37.2	80 2	86	hypothetical protein
1704	5204	1631745	1631353	393						
1705	5205	1631933	1633324	1392	gp AE002515_9	Neisseria meningitidis MC58 NMB1652	61.2	86.1	446	hypothetical protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
1706	5206	1632588	1632109	480	GSP:Y38838	Neisseria gonorrhoeae ORF24	54.0	60.0	113	antigenic protein
1707	5207	1633137	1632682	456	GSP:Y38838	Neisseria gonorrhoeae	59.0	69.0	152	antigenic protein
1708	5208	1633566	1636241	2676	sp:ATA1_SYNY3	Synechocystis sp. PCC6803 sll1614 pma1	42.6	73.2	883	cation-transporting ATPase P
1709	5209	1634563	1633781	783						
1710	5210	1636732	1636244	489	gp:SC3D11_2	Streptomyces coelicolor A3(2) SC3D11.02c	35.8	58.3	120	hypothetical protein
1711	5211	1637081	1638442	1362						
1712	5212	1639132	1638776	357						
1713	5213	1639365	1639520	156						
1714	5214	1639656	1639817	162						
1715	5215	1639781	1640155	375	prf:2408488H	Streptococcus thermophilus phage TP-J34	43.0	73.8	107	host cell surface-exposed lipoprotein
1716	5216	1640546	1641001	456	prf:2510491A	Corynephage 304L int	34.4	60.4	154	integrase
1717	5217	1642674	1641046	1629	sp:YJJK_ECOLI	Escherichia coli K12 yjjK	32.8	64.4	497	ABC transporter ATP-binding protein
1718	5218	1644218	1642743	1476						
1719	5219	1645499	1644318	1182	sp:NANH_MICVI	Micromonospora viridifaciens ATCC 31146 nedA	51.9	72.4	387	sialidase
1720	5220	1645661	1646368	708	gp:AF121000_8	Corynebacterium glutamicum 22243 R-plasmid pAG1 tnpB	99.6	100.0	236	transposase (IS1628)
1721	5221	1645821	1646063	243	GP:AF164956_23	Corynebacterium glutamicum TnpNC	64.0	72.0	37	transposase protein fragment
1722	5222	1645861	1645601	261	GP:NT1TNIS_5	Plasmid NTP16	32.0	43.0	88	hypothetical protein
1723	5223	1646549	1647133	585						
1724	5224	1647634	1647212	423	pir:B75015	Pyrococcus abyssi Orsay PAB1087	32.7	70.1	107	dTDP-4-keto-L-rhamnose reductase
1725	5225	1648097	1647651	447	pir:S72754	Mycobacterium leprae MLCL536.24c nifU7	63.8	85.2	149	nitrogen fixation protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1726	5226	1648548	1648709	162	PIR C72506	Aeropyrum pernix K1 APE2025	48.0	57.0	52	hypothetical protein
1727	5227	1649362	1648100	1263	pir S72761	Mycobacterium leprae nifS	64.7	84.4	411	nitrogen fixation protein
1728	5228	1650122	1649367	756	gp SCC22_4	Streptomyces coelicolor A3(2) SCC22.04c	70.2	89.3	252	ABC transporter ATP-binding protein
1729	5229	1651424	1650249	1176	pir A70872	Mycobacterium tuberculosis H37Rv Rv1462	55.2	83.0	377	hypothetical protein
1730	5230	1652875	1651433	1443	sp Y074_SYNY3	Synechocystis sp. PCC6803 slr0074	41.0	73.0	493	ABC transporter
1731	5231	1653586	1652894	693	gp SCC22_8	Streptomyces coelicolor A3(2) SCC22.08c	46.1	71.4	217	DNA-binding protein
1732	5232	1654043	1655671	1629	pir F70871	Mycobacterium tuberculosis H37Rv Rv1459c	36.3	67.8	518	hypothetical membrane protein
1733	5233	1655681	1656700	1020	pir S72783	Mycobacterium leprae MLCL536.31 abc2	50.2	77.3	317	ABC transporter
1734	5234	1656712	1657515	804	pir S72778	Mycobacterium leprae MLCL536.32	41.0	74.8	266	hypothetical protein
1735	5235	1657677	1658675	999	pir C70871	Mycobacterium tuberculosis H37Rv Rv1456c	43.0	74.6	291	hypothetical protein
1736	5236	1659496	1659140	357						
1737	5237	1659508	1661136	1629	pir C71156	Pyrococcus horikoshii PH0450	23.4	51.0	418	helicase
1738	5238	1661578	1662552	975	sp QOR_ECOLI	Escherichia coli K12 qor	37.5	70.9	323	quinone oxidoreductase
1739	5239	1663506	1662630	969	gp NWCOXABC_3	Nitrobacter winogradskyi coxC	37.6	66.8	295	cytochrome o ubiquinol oxidase assembly factor / heme O synthase
1740	5240	1664403	1666502	2100	gp AB023377_1	Corynebacterium glutamicum ATCC 31833 tkt	100.0	100.0	675	transketolase
1741	5241	1666673	1667752	1080	sp TAL_MYCLE	Mycobacterium leprae MLCL536.39 tal	62.0	85.2	358	transaldolase
1742	5242	1667764	1666601	1164						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1743	5243	1667950	1669401	1452	gsp W27612	Brevibacterium flavum	99 8	100 0	484	glucose-6-phosphate dehydrogenase
1744	5244	1669419	1670375	957	pir A70917	Mycobacterium tuberculosis H37Rv Rv1446c opcA	40 6	71 7	318	oxppcycle protein (glucose 6 phosphate dehydrogenase assembly protein)
1745	5245	1670395	1671099	705	sp SOL3_YEAST	Saccharomyces cerevisiae S288C YHR163W so3	28 7	58 1	258	6-phosphogluconolactonase
1746	5246	1671677	1671273	405	sp SAOX_BACSN	Bacillus sp. NS-129	35 2	57 8	128	sarcosine oxidase
1747	5247	1671723	1673123	1401	gp AF126281_1	Rhodococcus erythropolis	24 6	46 6	500	transposase (IS1676)
1748	5248	1674105	1673266	840	gp CGL007732_5	Corynebacterium glutamicum ATCC 13032 soxA	100 0	100 0	205	sarcosine oxidase
1749	5249	1677211	1677384	174						
1750	5250	1678756	1678070	687						
1751	5251	1679148	1680128	981						
1752	5252	1681108	1680332	777	sp TPIS_CORGL	Corynebacterium glutamicum AS019 ATCC 13059 tpiA	99 2	99 6	259	triose-phosphate isomerase
1753	5253	1681263	1681670	408	SP YCQ3_YEAST	Saccharomyces cerevisiae YCR013c	37 0	51 0	128	probable membrane protein
1754	5254	1682404	1681190	1215	sp PGK_CORGL	Corynebacterium glutamicum AS019 ATCC 13059 pgk	98 0	98 5	405	phosphoglycerate kinase
1755	5255	1683025	1682624	1002	sp G3P_CORGL	Corynebacterium glutamicum AS019 ATCC 13059 gap	99 1	99 7	333	glyceraldehyde-3-phosphate dehydrogenase
1756	5256	1685097	1684117	981	pir D70903	Mycobacterium tuberculosis H37Rv Rv1423	63 9	87 4	324	hypothetical protein
1757	5257	1686132	1685110	1023	sp YR40_MYCTU	Mycobacterium tuberculosis H37Rv Rv1422	56 3	82 5	309	hypothetical protein
1758	5258	1687078	1686152	927	sp YR39_MYCTU	Mycobacterium tuberculosis H37Rv Rv1421	52 0	76 2	281	hypothetical protein
1759	5259	1689190	1687103	2088	sp UVRC_PSEFL	Synechocystis sp PCC6803 uvrC	34 4	61 5	701	excinuclease ABC subunit C

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1760	5260	1689779	1689201	579	sp YR35_MYCTU	Mycobacterium tuberculosis H37Rv Rv1417	32.7	68.7	150	hypothetical protein
1761	5261	1690345	1689869	477	sp RISB_ECOLI	Escherichia coli K12	43.5	72.1	154	6,7-dimethyl-8-ribityllumazine synthase
1762	5262	1690694	1690921	228	GSP Y83273	Bacillus subtilis	59.0	68.0	72	polypeptide encoded by rib operon
1763	5263	1690708	1691421	714	GSP Y83272	Bacillus subtilis	26.0	48.0	217	riboflavin biosynthetic protein
1764	5264	1691012	1691347	336	GSP Y83273	Bacillus subtilis	44.0	52.0	106	polypeptide encoded by rib operon
1765	5265	1691625	1690360	1266	gp AF001929_1	Mycobacterium tuberculosis ribA	65.6	84.7	404	GTP cyclohydrolase II and 3, 4-dihydroxy-2-butanone 4-phosphate synthase (riboflavin synthesis)
1766	5266	1692271	1691639	633	sp RISA_ACTPL	Actinobacillus pleuropneumoniae ISU-178 ribE	47.4	79.2	211	riboflavin synthase alpha chain
1767	5267	1693258	1692275	984	sp RIBD_ECOLI	Escherichia coli K12 ribD	37.3	62.7	365	riboflavin-specific deaminase
1768	5268	1693918	1693262	657	sp RPE_YEAST	Saccharomyces cerevisiae S288C YJL121C rpe1	43.6	73.1	234	ribulose-phosphate 3-epimerase
1769	5269	1695298	1693967	1332	sp SUN_ECOLI	Escherichia coli K12 sun	30.8	60.7	448	nucleolar protein NOL1/NOP2 (eukaryotes) family
1770	5270	1696443	1695499	945	sp FMT_PSEAE	Pseudomonas aeruginosa fmt	41.6	67.9	308	methionyl-tRNA formyltransferase
1771	5271	1696972	1696466	507	sp DEF_BACSU	Bacillus subtilis 168 def	44.7	72.7	150	polypeptide deformylase
1772	5272	1699147	1697084	2064	sp PRIA_ECOLI	Escherichia coli priA	22.9	46.3	725	primosomal protein n'
1773	5273	1700397	1699177	1221	gsp R80060	Brevibacterium flavum MJ-233	99.3	99.5	407	S-adenosylmethionine synthetase
1774	5274	1701757	1700508	1260	sp DFP_MYCTU	Mycobacterium tuberculosis H37Rv RV1391 dfp	58.0	80.9	409	DNA/pantothenate metabolism flavoprotein
1775	5275	1702322	1702032	291	sp YD90_MYCTU	Mycobacterium tuberculosis H37Rv Rv1390	70.4	87.7	81	hypothetical protein
1776	5276	1703037	1702411	627	pir KIBYGU	Saccharomyces cerevisiae guk1	39.8	74.7	186	guanylate kinase
1777	5277	1703308	1702991	318	pir B70899	Mycobacterium tuberculosis H37Rv Rv1388 mIHF	80.6	90.3	103	integration host factor

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1778	5278	1704350	1703517	834	sp DCOP_MYCTU	Mycobacterium tuberculosis H37Rv uraA	51.8	73.6	276	orotidine 5' phosphate decarboxylase
1779	5279	1707697	1704359	3339	pir SYECCP	Escherichia coli carB	53.1	77.5	1122	carbamoyl-phosphate synthase large chain
1780	5280	1708881	1707706	1173	sp CARA_PSEAE	Pseudomonas aeruginosa ATCC 15692 carA	45.4	70.1	381	carbamoyl-phosphate synthase small chain
1781	5281	1710357	1709017	1341	sp PYRC_BACCL	Bacillus caldolyticus DSM 405 pyrC	42.8	67.7	402	dihydrocorotase
1782	5282	1711348	1710413	936	sp PYRB_PSEAE	Pseudomonas aeruginosa ATCC 15692	48.6	79.7	311	aspartate carbamoyltransferase
1783	5283	1711927	1711352	576	sp PYRR_BACCL	Bacillus caldolyticus DSM 405 pyrR	54.0	80.1	176	phosphoribosyl transferase of pyrimidine operon regulatory protein
1784	5284	1712596	1713759	1164	sp Y00R_MYCTU	Mycobacterium tuberculosis H37Rv Rv2216	39.7	73.4	297	cell division inhibitor
1785	5285	1713830	1714306	477						
1786	5286	1714299	1714760	462						
1787	5287	1714741	1714950	210						
1788	5288	1716052	1715382	681	sp NUSB_BACSU	Bacillus subtilis nusB	33.6	69.3	137	N utilization substance protein B (regulation of rRNA biosynthesis by transcriptional antitermination)
1789	5289	1716692	1716132	561	sp EFP_BRELA	Brevibacterium lactofermentum ATCC 13869 efp	97.9	98.4	187	elongation factor P
1790	5290	1717868	1716780	1089	gp AF124600_4	Corynebacterium glutamicum AS019 pepQ	99.5	100.0	217	cytoplasmic peptidase
1791	5291	1719032	1717938	1095	gp AF124600_3	Corynebacterium glutamicum AS019 aroB	98.6	99.7	361	3-dehydroquinate synthase
1792	5292	1719598	1719107	492	gp AF124600_2	Corynebacterium glutamicum AS019 aroK	100.0	100.0	166	shikimate kinase
1793	5293	1721381	1720971	411	sp LEP3_AERHY	Aeromonas hydrophila tapD	35.2	54.9	142	type IV prepilin-like protein specific leader peptidase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1794	5294	1721725	1721423	303	gp SC1A2_22	Streptomyces coelicolor A3(2) SC1A2.22	45.8	68.7	83	bacterial regulatory protein, arsR family
1795	5295	1721780	1722853	1074	gp AF109162_2	Corynebacterium diphtheriae hmuU	35.9	73.2	340	ABC transporter
1796	5296	1722807	1722202	606						
1797	5297	1722870	1723826	957	pir A75169	Pyrococcus abyssi Orsay PAB0349	23.6	50.7	373	iron(III) ABC transporter, periplasmic-binding protein
1798	5298	1723826	1724578	753	sp FHUC_BACSU	Bacillus subtilis 168 fhuC	38.3	71.7	230	ferrichrome transport ATP-binding protein
1799	5299	1725439	1724613	828	pir D70660	Mycobacterium tuberculosis H37Rv aroE	50.0	60.0	259	shikimate 5-dehydrogenase
1800	5300	1726625	1725459	1167	pir E70660	Mycobacterium tuberculosis H37Rv Rv2553c	41.8	70.1	395	hypothetical protein
1801	5301	1727170	1726625	546	pir F70660	Mycobacterium tuberculosis H37Rv Rv2554c	52.8	69.6	161	hypothetical protein
1802	5302	1730048	1727385	2664	sp SYA_THIFE	Thiobacillus ferrooxidans ATCC 33020 alaS	43.3	71.8	894	alanyl-tRNA synthetase
1803	5303	1731542	1730166	1377	sp Y0A9_MYCTU	Mycobacterium tuberculosis H37Rv Rv2559c	65.4	84.8	454	hypothetical protein
1804	5304	1732822	1731599	1224						
1805	5305	1734811	1732988	1824	sp SYD_MYCLE	Mycobacterium leprae aspS	71.1	89.2	591	aspartyl-tRNA synthetase
1806	5306	1735056	1735946	891	sp Y0BQ_MYCTU	Mycobacterium tuberculosis H37Rv Rv2575	46.1	74.1	297	hypothetical protein
1807	5307	1738679	1736004	2676	sp AMYH_YEAST	Saccharomyces cerevisiae S288C YIR019C sta1	26.1	53.6	839	glucan 1,4-alpha-glucosidase
1808	5308	1740559	1738713	1857	sp YHGE_BACSU	Bacillus subtilis yhgE	23.1	54.0	742	phage infection protein
1809	5309	1741219	1740572	648						
1810	5310	1741313	1741906	594	gp SCE68_13	Streptomyces coelicolor A3(2) SCE68.13	29.2	62.0	192	transcriptional regulator

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1811	5311	1741893	1742606	714						
1812	5312	1742701	1743813	1113	gp SCE15_13	Streptomyces coelcolor A3(2) SCE15.13c	72.8	88.1	371	oxidoreductase
1813	5313	1743843	1743968	126						
1814	5314	1744025	1744519	495	sp SLFA_PSEAE	Pseudomonas aeruginosa PAO1 slfA	37.1	77.6	116	NADH-dependent FMN reductase
1815	5315	1744884	1746230	1347	sp SDHL_ECOLI	Escherichia coli K12 sdaA	46.8	71.4	462	L-serine dehydratase
1816	5316	1746728	1747588	861						
1817	5317	1747918	1746233	1686	prf 2423362A	Enterococcus casseliflavus glpO	28.4	53.9	598	alpha-glycerolphosphate oxidase
1818	5318	1749276	1747990	1287	sp SYH_STAAU	Staphylococcus aureus SR17238 hisS	43.2	72.2	421	histidyl-tRNA synthetase
1819	5319	1749963	1749325	639	gp CJ11168X3_127	Campylobacter jejuni NCTC11168 Cj0809c	40.3	62.1	211	hydrolase
1820	5320	1750427	1750933	507	prf 2313309A	Streptomyces chrysomallus sccypB	35.4	61.1	175	cyclophilin
1821	5321	1750964	1751200	237						
1822	5322	1751497	1752051	555	gp AF038651_4	Corynebacterium glutamicum ATCC 13032 orf4	98.4	100.0	128	hypothetical protein
1823	5323	1752186	1752527	342						
1824	5324	1754894	1752615	2280	gp AF038651_3	Corynebacterium glutamicum ATCC 13032 rel	99.9	99.9	760	GTP pyrophosphokinase
1825	5325	1755479	1754925	555	gp AF038651_2	Corynebacterium glutamicum ATCC 13032 apt	99.5	100.0	185	adenine phosphoribosyltransferase
1826	5326	1755748	1755599	150	gp AF038651_1	Corynebacterium glutamicum ATCC 13032 dciAE	98.0	98.8	49	dipeptide transport system
1827	5327	1757228	1755486	1743	sp Y0BG_MYCTU	Mycobacterium tuberculosis H37Rv Rv2585c	30.7	60.9	558	hypothetical protein
1828	5328	1758797	1757589	1209	sp SECF_ECOLI	Escherichia coli K12 secF	25.9	57.2	332	protein export membrane protein
1829	5329	1759707	1760336	630						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
1830	5330	1760734	1758803	1932	prf.2313285A	Rhodobacter capsulatus secD	24.4	52.0	616	protein-export membrane protein
1831	5331	1761367	1761005	363	sp.Y0BD_MYCLE	Mycobacterium leprae MLCB1259.04	39.6	66.0	106	hypothetical protein
1832	5332	1762438	1761419	1020	sp.RUVB_ECOLI	Escherichia coli K12 ruvB	55.3	81.9	331	holliday junction DNA helicase
1833	5333	1763134	1762517	618	sp.RUVA_MYCLE	Mycobacterium leprae ruvA	45.2	74.3	210	holliday junction DNA helicase
1834	5334	1763839	1763177	663	sp.RUVC_ECOLI	Escherichia coli K12 ruvC	35.6	63.3	180	crossover junction endodeoxyribonuclease
1835	5335	1764742	1763990	753	sp.YEBC_ECOLI	Escherichia coli K12 ORF246 yebC	49.2	78.4	250	hypothetical protein
1836	5336	1765860	1765015	846	sp.TESB_ECOLI	Escherichia coli K12 tesB	38.5	68.6	283	acyl-CoA thiolesterase
1837	5337	1765969	1765442	474	gp.SC10A5_9	Streptomyces coelicolor A3(2) SC10A5.09c	31.5	61.3	111	hypothetical protein
1838	5338	1766948	1766487	462	pir.H70570	Mycobacterium tuberculosis H37Rv Rv2609c	38.2	61.2	170	hypothetical protein
1839	5339	1768030	1766948	1083	sp.GPI3_YEAST	Saccharomyces cerevisiae S288C spt14	21.7	49.3	414	hexosyltransferase or N-acetylglucosaminyl-phosphatidylinositol biosynthetic protein
1840	5340	1768996	1768034	963	gp.SCL2_16	Streptomyces coelicolor A3(2) SCL2.16c	46.4	67.8	295	acyltransferase
1841	5341	1769678	1769022	657	pir.C70571	Mycobacterium tuberculosis H37Rv Rv2612c pgsA	48.2	78.0	78	CDP-diacylglycerol--glycerol-3-phosphate phosphatidyltransferase
1842	5342	1770340	1769681	660	pir.D70571	Mycobacterium tuberculosis H37Rv Rv2613c	54.6	78.4	194	histidine triad (HIT) family protein
1843	5343	1772384	1770327	2058	sp.SYT2_BACSU	Bacillus subtilis thrZ	42.0	68.9	647	threonyl-tRNA synthetase
1844	5344	1773863	1772658	1206	sp.YWBN_BACSU	Bacillus subtilis ywbN	34.3	61.8	400	hypothetical protein
1845	5345	1773881	1774444	564						
1846	5346	1774438	1773893	545						
1847	5347	1775191	1774457	735						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1848	5348	1777269	1777646	378						
1849	5349	1777444	1778037	594						
1850	5350	1779508	1778102	1407						
1851	5351	1780168	1779554	615						
1852	5352	1780905	1780507	399						
1853	5353	1781585	1781019	567	sp PUAC_STRLP	Streptomyces anulatus pac	36.3	54.2	190	puromycin N-acetyltransferase
1854	5354	1781705	1782790	1086						
1855	5355	1783281	1784381	1101						
1856	5356	1784080	1783382	699						
1857	5357	1785473	1782894	2580						
1858	5358	1786844	1785732	1113						
1859	5359	1788829	1786907	1923						
1860	5360	1789080	1789562	483						
1861	5361	1789580	1789768	189						
1862	5362	1789746	1790057	312						
1863	5363	1790889	1790461	429						
1864	5364	1791842	1792438	597	sp AFUC_ACTPI	Actinobacillus pleuropneumoniae afuC	28.7	28.7	202	ferric transport ATP-binding protein
1865	5365	1792428	1793426	999						
1866	5366	1793654	1793496	159						
1867	5367	1793714	1794820	1107						
1868	5368	1795202	1795621	420						
1869	5369	1795591	1796181	591	gp AF088896_20	Zymomonas mobilis dfp	27.1	66.7	129	pantothenate metabolism flavoprotein
1870	5370	1796186	1797049	864						
1871	5371	1797350	1797769	420						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1872	5372	1797969	1797850	120						
1873	5373	1798757	1798023	735						
1874	5374	1799182	1799406	225						
1875	5375	1799473	1800366	894						
1876	5376	1800604	1800449	156						
1877	5377	1800834	1801307	474						
1878	5378	1801344	1802090	753						
1879	5379	1802577	1802155	423						
1880	5380	1802733	1803419	687						
1881	5381	1803465	1803893	429						
1882	5382	1804134	1804598	465						
1883	5383	1804629	1804865	237						
1884	5384	1804919	1805599	681						
1885	5385	1805727	1806686	960						
1886	5386	1806917	1807396	480						
1887	5387	1807433	1808113	681						
1888	5388	1808137	1808421	285						
1889	5389	1808458	1808832	375						
1890	5390	1809761	1810372	612	sp TNP2_ECOLI	Escherichia coli tnpR	51.1	78.0	186	transposon TN21 resolvase
1891	5391	1810541	1811545	1005						
1892	5392	1811564	1811938	375						
1893	5393	1812215	1812691	477	sp PVH1_YEAST	Saccharomyces cerevis ae S288C YIR026C yvh1	29.3	51.8	164	protein-tyrosine phosphatase
1894	5394	1812881	1813606	726						
1895	5395	1812882	1812460	423						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1896	5396	1813780	1814517	738	gp SCA32WHIH_6	Streptomyces coelicolor A3(2) whiH	34 3	65 7	216	sporulation transcription factor
1897	5397	1814863	1815651	789						
1898	5398	1815673	1816128	456						
1899	5399	1816451	1816636	186						
1900	5400	1817132	1817803	672						
1901	5401	1817803	1818219	417						
1902	5402	1818460	1818774	315						
1903	5403	1818798	1819166	369						
1904	5404	1819954	1819748	207						
1905	5405	1822382	1820181	2202	pir C72285	Thermotoga maritima MSB8 TM1189	22 6	55 2	545	hypothetical protein
1906	5406	1822577	1824322	1746						
1907	5407	1824371	1824589	219						
1908	5408	1824784	1824927	144						
1909	5409	1825606	1825178	429						
1910	5410	1826024	1826557	534	PIR S60891	Corynebacterium glutamicum	63 0	75 0	166	hypothetical protein
1911	5411	1826644	1825751	894	pir S60890	Corynebacterium glutamicum orf2	87 9	95 6	298	insertion element (IS3 related)
1912	5412	1826937	1826644	294	pir S60889	Corynebacterium glutamicum orf1	72 3	84 2	101	insertion element (IS3 related)
1913	5413	1829900	1829688	213						
1914	5414	1830765	1832063	1299						
1915	5415	1832167	1834044	1878	sp RECJ_ERWCH	Erwinia chrysanthemi recJ	24 0	50 6	622	single-stranded-DNA-specific exonuclease
1916	5416	1834028	1834149	780						
1917	5417	1836675	1838324	1650	pir I13302	Streptococcus phage phi-O1205 ORF13	31 8	64 3	381	primase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1918	5418	1838349	1842137	3789						
1919	5419	1842235	1842681	447						
1920	5420	1842804	1843337	534						
1921	5421	1843518	1845356	1839	sp YC18_MYCPN	Mycoplasma pneumoniae ATCC 29342 yb95	22.1	44.7	620	helicase
1922	5422	1845483	1845857	375						
1923	5423	1845872	1846207	336	pir T13144	Bacteriophage N15 gene57	36.7	64.2	109	phage N15 protein gp57
1924	5424	1846698	1846333	366						
1925	5425	1847315	1847932	618						
1926	5426	1847938	1848474	537						
1927	5427	1848509	1849036	528						
1928	5428	1848988	1849785	798						
1929	5429	1849781	1849966	186						
1930	5430	1850035	1850406	372						
1931	5431	1850415	1849978	438						
1932	5432	1851049	1850474	576						
1933	5433	1851220	1852440	1221	gp SPAPJ760_2	Schizosaccharomyces pombe SPAPJ760 02c	28.7	49.8	422	actin binding protein with SH3 domains
1934	5434	1851473	1852324	852						
1935	5435	1852479	1853873	1395						
1936	5436	1854261	1854854	594						
1937	5437	1855058	1855237	180						
1938	5438	1855532	1856788	1257	gp SC5C7_14	Streptomyces coelicolor SC5C7.14	23.6	52.5	347	ATP/GTP binding protein
1939	5439	1856885	1858738	1854						
1940	5440	1858763	1860727	1965	sp CLPA_ECOLI	Escherichia coli K12 clpA	39.2	61.0	630	ATP-dependent Clp proteinase ATP-binding subunit

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
1941	5441	1860752	1861225	474						
1942	5442	1861320	1861475	156						
1943	5443	1861842	1861519	324						
1944	5444	1862088	1862399	312						
1945	5445	1862945	1865299	2355	sp:PCRA_STAAU	Staphylococcus aureus SA20 pcrA	21.4	45.9	693	ATP-dependent helicase
1946	5446	1865265	1865822	558						
1947	5447	1865842	1866219	378						
1948	5448	1866328	1866792	465						
1949	5449	1866832	1867095	264						
1950	5450	1867098	1867874	777	gp:SCH17_7	Streptomyces coelicolor A3(2) SCH17.07c	25.9	47.8	224	hypothetical protein
1951	5451	1867886	1868587	702	prf:2514444Y	Bacteriophage phi-C31 gp52	31.7	61.5	208	deoxynucleotide monophosphate kinase
1952	5452	1868895	1868671	225						
1953	5453	1871092	1868927	2166						
1954	5454	1871373	1871101	273						
1955	5455	1877886	1871380	6507						
1956	5456	1878312	1879400	1089	prf:2403350A	Corynebacterium glutamicum ATCC 13032 cglIM	99.2	99.7	363	type II 5-cytosine methyltransferase
1957	5457	1879412	1880485	1074	pir:A55225	Corynebacterium glutamicum ATCC 13032 cglIR	99.7	99.7	358	type II restriction endonuclease
1958	5458	1883990	1882470	1521						
1959	5459	1884936	1884220	717						
1960	5460	1885230	1887047	1818	gp:SC1A2_16	Streptomyces coelicolor A3(2) SC1A2.16c	24.6	45.8	504	hypothetical protein
1961	5461	1887405	1887590	186						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1962	5462	1888036	1887688	351	gp AE001973_4	Deinococcus radiodurans DR1258	46.7	70.0	90	SNF2/Rad54 helicase-related protein
1963	5463	1889094	1888231	864	pir T13226	Lactobacillus phage phi-gle Rorf232	33.1	56.4	163	hypothetical protein
1964	5464	1889530	1889859	330						
1965	5465	1891707	1890028	1680	gp AF188935_16	Bacillus anthracis pXO2-16	20.7	47.9	537	hypothetical protein
1966	5466	1893037	1891832	1206						
1967	5467	1894680	1893388	1293						
1968	5468	1897231	1894739	2493						
1969	5469	1899158	1897374	1785	sp CLPB_ECOLI	Escherichia coli clpB	25.3	52.5	724	endopeptidase Clp ATP-binding chain B
1970	5470	1899853	1899233	621						
1971	5471	1900916	1899804	1113						
1972	5472	1901911	1901066	846						
1973	5473	1901975	1902955	981						
1974	5474	1902883	1902005	879						
1975	5475	1903028	1903225	198						
1976	5476	1905878	1903113	2766	pir S23647	Homo sapiens numA	20.1	49.1	1004	nuclear mitotic apparatus protein
1977	5477	1906572	1905973	600						
1978	5478	1907914	1906664	1251						
1979	5479	1908660	1907965	696						
1980	5480	1909498	1908785	714						
1981	5481	1910508	1909501	1008						
1982	5482	1912300	1910642	1659						
1983	5483	1913820	1912333	1488						
1984	5484	1914371	1913973	399						
1985	5485	1916233	1914725	1509						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
1986	5486	1916374	1916733	360						
1987	5487	1916944	1917165	222						
1988	5488	1917040	1917329	312						
1989	5489	1918208	1917564	645						
1990	5490	1919461	1918703	759						
1991	5491	1920194	1919646	549						
1992	5492	1921276	1920347	930						
1993	5493	1925390	1925695	306						
1994	5494	1925682	1926038	357						
1995	5495	1926010	1921547	4464	pir T03099	Sus scrofa domestica	23 2	49 2	1408	submaxillary apomucin
1996	5496	1926837	1926259	579						
1997	5497	1928189	1927245	945						
1998	5498	1928211	1928381	171	sp MTE1_ECOLI	Escherichia coli ecoR1	42 6	65 6	61	modification methylase
1999	5499	1928534	1928908	375						
2000	5500	1930879	1929059	1821						
2001	5501	1931190	1930990	201						
2002	5502	1931888	1931421	468						
2003	5503	1932315	1931935	381	pir H70638	Mycobacterium tuberculosis H37Rv Rv1956	38 6	58 8	114	hypothetical protein
2004	5504	1932879	1932373	507						
2005	5505	1934358	1933522	837						
2006	5506	1935912	1934971	942	sp Y137_METJA	Methanococcus jannaschii MJ0137	27.1	54.6	328	hypothetical protein
2007	5507	1936226	1936849	624						
2008	5508	1937202	1937411	210						
2009	5509	1938019	1937485	534						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	nitial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2010	5510	1938945	1940135	1191						
2011	5511	1939064	1938531	534						
2012	5512	1940257	1940844	588						
2013	5513	1941107	1941550	444						
2014	5514	1942484	1941732	753						
2015	5515	1942510	1942812	303						
2016	5516	1943095	1943310	216						
2017	5517	1943345	1943653	309						
2018	5518	1943680	1944564	885						
2019	5519	1945435	1944608	828	prf 2509434A	Enterococcus faecalis esp	23.0	44.1	304	surface protein
2020	5520	1945891	1945595	297						
2021	5521	1946332	1945952	381						
2022	5522	1947037	1946609	429						
2023	5523	1948550	1947070	1581	sp CSP1_CORGL	Corynebacterium glutamicum (Brevibacterium flavum) ATCC 17965 csp1	30.7	54.4	270	major secreted protein PS1 protein precursor
2024	5524	1951450	1949021	2430						
2025	5525	1952485	1951619	867						
2026	5526	1954822	1952546	2277	sp TOP3_ECOLI	Escherichia coli topB	23.8	50.9	597	DNA topo somerase III
2027	5527	1958287	1956203	2085						
2028	5528	1959340	1958450	891						
2029	5529	1960196	1959765	432						
2030	5530	1961114	1960371	744						
2031	5531	1963000	1961114	1887	sp CSP1_CORGL	Corynebacterium glutamicum (Brevibacterium flavum) ATCC 17965 csp1	29.7	54.7	344	major secreted protein PS1 protein precursor
2032	5532	1963429	1963139	291						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (aa)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (aa)	Function
2033	5533	1964743	1963514	1230						
2034	5534	1965902	1964727	1176						
2035	5535	1966267	1965911	357						
2036	5536	1966301	1966984	684	sp NUC_STAAU	Staphylococcus aureus nuc	30 4	57 7	227	thermonuclease
2037	5537	1967435	1967269	147						
2038	5538	1967604	1968167	564						
2039	5539	1968264	1969715	1452						
2040	5540	1969745	1970203	459						
2041	5541	1970254	1971474	1221						
2042	5542	1971672	1973090	1419						
2043	5543	1973147	1973737	591						
2044	5544	1973809	1974204	396						
2045	5545	1974267	1974503	237						
2046	5546	1975171	1975794	624	prf 2313347B	Shewanella sp ssb	24 9	59 1	225	single stranded DNA-binding protein
2047	5547	1975916	1976494	579						
2048	5548	1976522	1976983	462						
2049	5549	1977043	1977549	507						
2050	5550	1977742	1978323	582						
2051	5551	1978389	1978721	333						
2052	5552	1978660	1979217	558						
2053	5553	1979239	1979809	570						
2054	5554	1979974	1983985	912	sp S24D_ANOGA	Anopheles gambiae AgSP24D	25 7	52 6	249	serine protease
2055	5555	1980965	1981657	693						
2056	5556	1981663	1982028	366						
2057	5557	1982071	1982817	747						
2058	5558	1982091	1981912	180						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
2059	5559	1983186	1983548	363						
2060	5560	1983611	1983883	273						
2061	5561	1983918	1984181	264						
2062	5562	1984217	1984450	234						
2063	5563	1984387	1984728	342						
2064	5564	1985092	1985364	273						
2065	5565	1985373	1985071	303						
2066	5566	1986590	1985442	1149	sp:VINT_BPML5	Mycobacterium phage L5 int	29.6	55.9	406	integrase
2067	5567	1987896	1987507	390	gsp:R23011	Brevibacterium lactofermentum CGL2005 ISaB1	83.9	94.4	124	transposase (divided)
2068	5568	1988303	1987887	417	gsp:R23011	Brevibacterium lactofermentum CGL2005 ISaB1	70.9	84.6	117	transposase (divided)
2069	5569	1988383	1988589	207						
2070	5570	1988483	1988370	114	gsp:R21601	Brevibacterium lactofermentum CGL2005 ISaB1	80.7	96.8	31	transposition repressor
2071	5571	1988664	1988530	135	pir:S60889	Corynebacterium glutamicum orf1	74.4	88.4	43	insertion element (IS3 related)
2072	5572	1989605	1988778	828	gp:SCJ11_12	Streptomyces coelicolor A3(2) SCJ11.12	31.1	53.7	270	transposase
2073	5573	1990667	1991020	354						
2074	5574	1990764	1989874	891						
2075	5575	1991620	1991189	432						
2076	5576	1992538	1991795	744						
2077	5577	1994121	1992538	1584	sp:CSP1_CORGL	Corynebacterium glutamicum (Brevibacterium flavum) ATCC 17965 csp1	25.0	37.0	153	major secreted protein PS1 protein precursor
2078	5578	1995294	1994608	687	sp:VINT_BPML5	Mycobacterium phage L5 int	28.7	56.1	223	integrase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2079	5579	1996088	1995783	306	pir F64546	Helicobacter pylori 26695 HP0214	39.8	76.1	88	sodium dependent transporter
2080	5580	1996106	1996537	432	sp YXAA_BACSU	Bacillus subtilis yxaA	48.9	81.5	92	hypothetical protein
2081	5581	1996769	1997112	345						
2082	5582	1997168	1997503	336						
2083	5583	1997545	1998240	696	pir C70968	Mycobacterium tuberculosis H37Rv Rv2671 ribD	33.5	64.4	233	riboflavin biosynthesis protein
2084	5584	1998289	1999542	1254	pir E70968	Mycobacterium tuberculosis H37Rv Rv2673	42.5	71.9	384	potential membrane protein
2085	5585	1999542	1999949	408	gp AF128264_2	Streptococcus gordonii msrA	41.3	67.5	126	methionine sulfoxide reductase
2086	5586	2000132	1999707	426						
2087	5587	2001216	2000521	696	pir H70968	Mycobacterium tuberculosis H37Rv Rv2676c	55.2	77.2	232	hypothetical protein
2088	5588	2001489	2002112	624	pir C70528	Mycobacterium tuberculosis H37Rv Rv2680	55.7	78.6	201	hypothetical protein
2089	5589	2002072	2003334	1263	sp RND_HAEIN	Haemophilus influenzae Rd KW20 HI0390 rnd	25.9	52.8	371	ribonuclease D
2090	5590	2005309	2003402	1908	gp AB026631_1	Streptomyces sp. CL190 dxs	55.3	78.5	618	1-deoxy-D-xylulose-5-phosphate synthase
2091	5591	2006697	2005462	1236	pir B72298	Thermotoga maritima MSB8 TM1094	25.4	52.3	472	RNA methyltransferase
2092	5592	2006698	2006979	282						
2093	5593	2007637	2006777	861	pir C70530	Mycobacterium tuberculosis H37Rv Rv2696c	38.1	62.7	268	hypothetical protein
2094	5594	2008184	2007738	447	sp DUT_STRCO	Streptomyces coelicolor A3(2) SC2E9.09 dut	55.0	82.1	140	deoxyuridine 5'-triphosphate nucleotidohydrolase
2095	5595	2008250	2008798	549	pir E70530	Mycobacterium tuberculosis H37Rv Rv2698	46.0	70.7	150	hypothetical protein
2096	5596	2009082	2008876	207						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
2097	5597	2009570	2009280	291	pir|F70530	Mycobacterium tuberculosis H37Rv Rv2699c	58.0	81.0	100	hypothetical protein
2098	5598	2010539	2009724	816	sp|SUHB_ECOLI	Escherichia coli K12 suhB	38.4	68.2	198	extragenic suppressor protein
2099	5599	2010555	2011382	828	sp|PPGK_MYCTU	Mycobacterium tuberculosis H37Rv RV2702 ppgK	54.4	80.2	248	polyphosphate glucokinase
2100	5600	2011863	2013356	1494	prf|2204286A	Corynebacterium glutamicum sigA	98.0	98.6	500	sigma factor or RNA polymerase transcription factor
2101	5601	2015495	2014162	1335	sp|YRKO_BACSU	Bacillus subtilis yrkO	23.9	51.4	422	hypothetical membrane protein
2102	5602	2016121	2015585	537						
2103	5603	2017966	2016257	1710	sp|Y065_MYCTU	Mycobacterium tuberculosis H37Rv Rv2917	61.3	80.8	578	hypothetical protein
2104	5604	2018119	2018754	636	pir|H70531	Mycobacterium tuberculosis H37Rv Rv2709	32.3	59.1	127	hypothetical membrane protein
2105	5605	2018202	2017966	237	pir|G70531	Mycobacterium tuberculosis H37Rv Rv2708c	65.8	85.5	76	hypothetical protein
2106	5606	2018744	2020276	1533	gp|SCH5_8	Streptomyces coelicolor A3(2) SCH5.08c	33.5	61.2	523	transferase
2107	5607	2020293	2020724	432	prf|2204286C	Corynebacterium glutamicum ATCC 13869 ORF1	97.2	100.0	144	hypothetical protein
2108	5608	2022266	2022949	684	pir|I40339	Corynebacterium glutamicum ATCC 13869 dtxR	98.7	99.6	228	iron dependent repressor or diphtheria toxin repressor
2109	5609	2022546	2022313	234	GP|AF010134_1	Streptomyces aureofaciens	62.0	64.0	77	putative sporulation protein
2110	5610	2022959	2023945	987	sp|GALE_BRELA	Corynebacterium glutamicum ATCC 13869 (Brevibacterium lactofermentum) galE	99.1	99.1	329	UDP-glucose 4-epimerase
2111	5611	2025270	2023948	1323						
2112	5612	2025423	2026379	957	pir|E70532	Mycobacterium tuberculosis H37Rv Rv2714	45.3	79.0	305	hypothetical protein
2113	5613	2026404	2028043	2550	sp|MTR4_YEAST	Saccharomyces cerevisiae YJL050W dob1	24.4	50.7	661	ATP-dependent RNA helicase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2114	5614	2029177	2030157	981	sp OXYR_ECOLI	Escherichia coli oxyR	35 8	65 6	299	hydrogen peroxide inducible genes activator
2115	5615	2031365	2030277	1089						
2116	5616	2031478	2035383	3906	sp HRPA_ECOLI	Escherichia coli hrpA	49 2	76 2	1298	ATP-dependent helicase
2117	5617	2035880	2035431	450	gp SCAJ4870_3	Streptomyces clavuligerus ordR	61 4	86 2	145	regulatory protein
2118	5618	2036409	2035990	420						
2119	5619	2036812	2037507	696	sp LEXA_BACSU	Bacillus subtilis dinR	46 9	71 6	222	SOS regulatory protein
2120	5620	2037815	2038591	777	sp GATR_ECOLI	Escherichia coli K12 gatR	33 9	67 8	245	galactitol utilization operon repressor
2121	5621	2038591	2039550	960	gp SCE22_14	Streptomyces coelicolor A3(2) SCE22 14c	27 2	55 6	320	phosphofructokinase (fructose 1 phosphate kinase)
2122	5622	2041321	2039618	1704	sp PT1_BACST	Bacillus stearothermophilus ptsI	34 3	64 0	592	phosphoenolpyruvate-protein phosphotransferase
2123	5623	2041728	2042519	792	sp GLPR_ECOLI	Escherichia coli K12 glpR	20 7	62 6	262	glycerol-3-phosphate regulon repressor
2124	5624	2042513	2043503	990	sp K1PF_RHOCA	Rhodobacter capsulatus fruK	33 0	55 7	345	1-phosphofructokinase or 6 phosphofructokinase
2125	5625	2043736	2045571	1836	sp PTFB_ECOLI	Escherichia coli K12 fruA	43 0	69 6	549	PTS system, fructose-specific IIBC component
2126	5626	2045762	2046028	267	sp PTHP_BACST	Bacillus stearothermophilus XI-65-6 ptsH	37 0	71 6	81	phosphocarrier protein
2127	5627	2047295	2046714	582						
2128	5628	2048606	2047320	1287	sp PYRP_BACCL	Bacillus caldolyticus pyrP	39 1	70 5	407	uracil permease
2129	5629	2050107	2048650	1458	gp AF145049_8	Streptomyces fradiae orf11*	54 4	80 0	419	ATP/GTP-binding protein
2130	5630	2050321	2051106	786						
2131	5631	2051306	2051842	537						
2132	5632	2052675	2051845	831	sp DAPF_HAEIN	Haemophilus influenzae Rd KW20 HI0750 dapF	33 5	64 7	269	diaminopimelate epimerase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	nitial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
2133	5633	2053596	2052684	903	sp MIAA_ECOLI	Escherichia coli K12 miaA	40.0	68.7	300	tRNA delta-2-isopentenylpyrophosphate transferase
2134	5634	2054283	2053609	675						
2135	5635	2054403	2055761	1359	pir B70506	Mycobacterium tuberculosis H37Rv Rv273	48.5	75.7	445	hypothetical protein
2136	5636	2055743	2054724	1020						
2137	5637	2055765	2056787	1023						
2138	5638	2057788	2057120	669	pir C70506	Mycobacterium tuberculosis H37Rv Rv2732c	29.0	63.7	190	hypothetical membrane protein
2139	5639	2059420	2057855	1566	sp Y195_MYCLE	Mycobacterium leprae B2235_C2_195	68.4	86.4	494	hypothetical protein
2140	5640	2059774	2060499	726	sp GLUA_CORGL	Corynebacterium glutamicum ATCC 13032 gluA	99.6	99.6	242	glutamate transport ATP-binding protein
2141	5641	2060414	2060196	219	GSP:Y75358	Neisseria gonorrhoeae	66.0	73.0	71	Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics
2142	5642	2061629	2062312	684	sp GLUC_CORGL	Corynebacterium glutamicum ATCC 13032 gluC	100.0	100.0	225	glutamate transport system permease protein
2143	5643	2062441	2063259	819	sp GLUD_CORGL	Corynebacterium glutamicum (Brevibacterium flavum) ATCC 13032 gluD	99.3	99.6	273	glutamate transport system permease protein
2144	5644	2063894	2063298	597	sp RECX_MYCLE	Mycobacterium leprae recX	34.5	66.9	142	regulatory protein
2145	5645	2065927	2065394	534	pir A70878	Mycobacterium tuberculosis H37Rv Rv2738c	40.3	71.6	67	hypothetical protein
2146	5646	2066404	2065667	738						
2147	5647	2066566	2067141	576	sp BIOY_BACSH	Bacillus sphaericus bioY	33.0	61.4	197	biotin synthase
2148	5648	2067168	2067866	699	sp POTG_ECOLI	Escherichia coli K12 potG	33.2	69.5	223	putrescine transport ATP-binding protein
2149	5649	2067866	2068174	609	pir F69742	Bacillus subtilis ybaF	24.6	58.8	228	hypothetical membrane protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2150	5650	2068703	2069392	690	pir B6C176	Mycobacterium tuberculosis	41.7	78.5	228	hypothetical protein
2151	5651	2069383	2068556	828	sp 35KD_MYCTU	Mycobacterium tuberculosis H37Rv RV2744C	72.5	89.6	269	hypothetical protein (35kD protein)
2152	5652	2069936	2069616	321	pir H70878	Mycobacterium tuberculosis H37Rv Rv2745c	54.2	78.3	83	regulator (DNA binding protein)
2153	5653	2070512	2069997	516	sp CINA_STRPN	Streptococcus pneumoniae R6X cinA	41.8	68.5	165	competence damage induced proteins
2154	5654	2071121	2070519	603	prf 2421334D	Streptococcus pyogenes pgsA	38.8	72.5	160	phosphotidylglyccrophosphate synthase
2155	5655	2071315	2071599	285	pir T10688	Arabidopsis thaliana ATSP:T16I18.20	24.8	52.1	117	hypothetical protein
2156	5656	2071624	2071740	117	gp AF071810_1	Streptococcus pneumoniae DBL5 pspA	60.0	70.0	30	surface protein (Peumococcal surface protein A)
2157	5657	2072096	2072878	813						
2158	5658	2072905	2071799	1107	prf 2119295D	Escherichia coli terC	31.0	59.8	358	tellurite resistance protein
2159	5659	2076056	2073294	2763	sp SP3E_BACSU	Bacillus subtilis 168 spoIIIE	38.0	64.6	845	stage III sporulation protein E
2160	5660	2077024	2076392	633	gp SC4G6_14	Streptomyces coelicolor A3(2) SC4G6.14	33.3	61.0	216	hypothetical protein
2161	5661	2079275	2077122	2154	sp YOR4_CORGL	Corynebacterium glutamicum ATCC 13032 orf4	99.1	99.4	645	hypothetical protein
2162	5662	2081136	2080387	750	sp YDAP_BRELA	Corynebacterium glutamicum (Brevibacterium lactofermentum) ATCC 13869 orf2	99.2	99.6	250	hypothetical protein
2163	5663	2082115	2082813	699						
2164	5664	2082368	2082105	264						
2165	5665	2085190	2082932	2259	prf 2217311A	Streptomyces antibioticus gpsI	65.4	85.3	742	guanosine pentaphosphate synthetase
2166	5666	2085702	2085436	267	pir F69700	Bacillus subtilis rpsO	64.0	88.8	89	30S ribosomal protein S15
2167	5667	2086826	2085879	948	prf 2518365A	Leishmania major	35.1	63.3	319	nucleoside hydrolase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
2168	5668	2087941	2086919	1023	sp:RIBF_CORAM	Corynebacterium ammoniagenes ATCC 6872 ribF	56.2	79.0	329	bifunctional protein (riboflavin kinase and FAD synthetase)
2169	5669	2087073	2088863	891	sp:TRUB_BACSU	Bacillus subtilis 168 truB	32.7	61.7	303	tRNA pseudouridine synthase B
2170	5670	2088181	2087954	228	PIR:PC4007	Corynebacterium ammoniagenes	65.0	73.0	47	hypothetical protein
2171	5671	2089868	2089218	651	gp:SC5A7_23	Streptomyces coelicolor A3(2) SC5A7.23	42.2	62.5	237	hypothetical protein
2172	5672	2090564	2089861	804	pir:B70885	Mycobacterium tuberculosis H37Rv Rv2795c	46.9	68.9	273	phosphoesterase
2173	5673	2092055	2090751	1305	pir:G70693	Mycobacterium tuberculosis H37Rv Rv2836c dinF	51.0	78.8	433	DNA damaged inducible protein f
2174	5674	2093046	2092051	996	pir:H70693	Mycobacterium tuberculosis H37Rv Rv2837c	36.7	70.8	308	hypothetical protein
2175	5675	2093501	2093055	447	sp:RBFA_BACSU	Bacillus subtilis 168 rbfA	32.4	70.4	108	ribosome-binding factor A
2176	5676	2096723	2093712	3012	sp:IF2_STIAU	Stigmatella aurantiaca DW4 infB	37.7	62.9	1103	translation initiation factor IF-2
2177	5677	2097179	2096844	336	gp:SC5H4_29	Streptomyces coelicolor A3(2) SC5H4.29	44.6	66.3	83	hypothetical protein
2178	5678	2098375	2097380	996	sp:NUSA_BACSU	Bacillus subtilis 168 nusA	42.3	71.0	352	n-utilization substance protein (transcriptional termination/antitermination factor)
2179	5679	2098562	2099815	1254						
2180	5680	2098945	2098412	534	pir:E70588	Mycobacterium tuberculosis H37Rv Rv2842c	34.6	65.5	165	hypothetical protein
2181	5681	2100240	2101841	1602	sp:DPPE_BACSU	Bacillus subtilis 168 dppE	25.3	60.9	534	peptide-binding protein
2182	5682	2102023	2102946	924	sp:DPPB_ECOLI	Escherichia coli K12 dppB	37.7	69.4	337	peptidetransport system permease
2183	5683	2102975	2103973	999	prf:1709239C	Bacillus subtilis spo0KC	38.4	69.2	292	oligopeptide permease
2184	5684	2103973	2105703	1731	pir:H70788	Mycobacterium tuberculosis H37Rv Rv3663c dppD	57.6	81.3	552	peptidetransport system ABC-transporter ATP-binding protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2185	5685	2107564	2105801	1764	sp SYP_MYCTU	Mycobacterium tuberculosis H37Rv Rv2845c proS	67 0	84 6	578	prolyl-tRNA synthetase
2186	5686	2107652	2108386	735	gp SCC30_5	Streptomyces coelicolor A3(2) SCC30 05	39 5	65 0	243	hypothetical protein
2187	5687	2109147	2108389	759	sp BCHD_RHOSH	Rhodobacter sphaeroides ATCC 17023 bchD	32 4	60 7	37	magnesium-chelatase subunit
2188	5688	2110255	2109155	1101	prf 2503462AA	Heliobacillus mobilis bchI	46 5	69 6	342	magnesium-chelatase subunit
2189	5689	2111183	2110434	750	prf 2108318B	Propionibacterium freudenreichii cobA	49 0	73 8	237	uroporphyrinogen III methyltransferase
2190	5690	2111238	2112659	1422	sp YPLC_CLOPE	Clostridium perfringens NCIB 10662 ORF2	41 2	68 7	488	hypothetical protein
2191	5691	2113616	2112717	900	gp SC5H1_10	Streptomyces coelicolor A3(2) SC5H1 10c	35 1	62 3	151	hypothetical protein
2192	5692	2115791	2116774	1014	pir A70590	Mycobacterium tuberculosis H37Rv Rv2854	37 6	65 7	338	hypothetical protein
2193	5693	2116916	2118310	1395	sp GSHR_BURCE	Burkholderia cepacia AC1100 gor	53 0	76 6	466	glutathione reductase
2194	5694	2117956	2117015	942						
2195	5695	2118607	2119080	474						
2196	5696	2119139	2119495	357						
2197	5697	2119628	2120356	729						
2198	5698	2121147	2120359	789	sp AMPM_ECOLI	Escherichia coli K12 map	47.2	75 8	252	methionine aminopeptidase
2199	5699	2123161	2121296	1866	prf 2324268A	Streptomyces clavuligerus pcbR	27 3	56 5	630	penicillin binding protein
2200	5700	2123848	2123219	630	prf 2518330B	Corynebacterium diphtheriae chrA	44 0	72 2	216	response regulator (two component system response regulator)
2201	5701	2124996	2123848	1149	prf 2518330A	Corynebacterium diphtheriae chrS	29 5	56 6	424	two component system sensor histidine kinase
2202	5702	2125089	2126045	957	gp AE001863_70	Deinococcus radiodurans DRA0279	24 4	58 1	360	hypothetical membrane protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
2203	5703	2126064	2126753	690	prf 2420410B	Bacillus subtilis 168 yvrO	37.3	71.1	225	ABC transporter
2204	5704	2127087	2126926	162						
2205	5705	2128483	2127350	1134	sp GCPE_ECOLI	Escherichia coli K12 gcpE	44.3	73.8	359	hypothetical protein (gcpE protein)
2206	5706	2128850	2129461	612						
2207	5707	2129880	2129569	1212	pir G70886	Mycobacterium tuberculosis H37Rv Rv2869c	43.0	73.6	405	hypothetical membrane protein
2208	5708	2130396	2130950	645	GSP Y37145	Chlamydia trachomatis	36.0	43.0	147	polypeptides can be used as vaccines against Chlamydia trachomatis
2209	5709	2131078	2129903	1176	sp DXR_ECOLI	Escherichia coli K12 dxr	22.8	42.0	312	1-deoxy-D-xylulose-5-phosphate reductoisomerase
2210	5710	2131322	2131762	441						
2211	5711	2131726	2131247	480						
2212	5712	2133402	2131825	1578						
2213	5713	2134260	2133406	855	pir B72334	Thermotoga maritima MSB8 TM0793	37.1	75.1	245	ABC transporter ATP-binding protein
2214	5714	2135551	2134454	1098	sp YS80_MYCTU	Mycobacterium tuberculosis H37Rv	66.0	78.0	356	pyruvate formate-lyase 1 activating enzyme
2215	5715	2135894	2136141	258	pir A70801	Mycobacterium tuberculosis H37Rv Rv3760	41.5	74.5	94	hypothetical membrane protein
2216	5716	2137089	2136235	855	sp CDSA_PSEAE	Pseudomonas aeruginosa ATCC 15692 cdsA	33.3	56.5	294	phosphatidate cytidylyltransferase
2217	5717	2137840	2137286	555	sp RRF_BACSU	Bacillus subtilis 168 frr	47.0	84.3	185	ribosome recycling factor
2218	5718	2138654	2137935	720	prf 2510355C	Pseudomonas aeruginosa pyrH	28.4	43.1	109	uridylate kinase
2219	5719	2138994	2139854	861						
2220	5720	2139827	2139003	825	sp EFTS_STRCO	Streptomyces coelicolor A3(2) SCZE1.42 tsf	49.6	76.8	280	elongation factor Ts
2221	5721	2140886	2140071	816	pir A69693	Bacillus subtilis rpsB	54.7	83.5	254	30S ribosomal protein S2

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2222	5722	2141257	2141760	504	sp YS91_MYCTU	Mycobacterium tuberculosis H37Rv Rv2891	46 0	58 0	120	hypothet cal protein
2223	5723	2142686	2141763	924	prf 2417318A	Proteus mirabilis xerD	40 1	68 7	297	site specific recombinase
2224	5724	2144066	2142885	1182	sp YX27_MYCTU	Mycobacterium tuberculosis H37Rv Rv2896c	39 8	66 8	395	hypothetical protein
2225	5725	2145586	2144066	1521	sp YX28_MYCTU	Mycobacterium tuberculosis H37Rv Rv2897c	46 6	75 8	504	Mg(2+) chelatase family protein
2226	5726	2145941	2145579	366	sp YX29_MYCTU	Mycobacterium tuberculosis H37Rv Rv2898c	40 3	72 3	119	hypothetical protein
2227	5727	2146566	2146264	303	sp YTC1_MYCTU	Mycobacterium tuberculosis H37Rv Rv2901c	68 3	96 0	101	hypothetical protein
2228	5728	2147192	2146566	627	sp RNH2_HAEIN	Haemophilus influenzae Rd HI1059 rnhB	42 6	69 5	190	ribonuclease HII
2229	5729	2147231	2148022	792						
2230	5730	2148046	2147261	786	prf 2514288H	Streptomyces lividans TK21 sipY	32 3	61 1	285	signal peptidase
2231	5731	2148231	2149166	936	prf 2510361A	Staphylococcus aureus sirA	25 4	59 1	323	Fe-regulated protein
2232	5732	2149571	2149359	213						
2233	5733	2149972	2149634	339	sp RL19_BACST	Bacillus stearothermophilus rplS	70 3	88 3	111	50S ribosomal protein L19
2234	5734	2150335	2150997	663	sp THIE_BACSU	Bacillus subtilis 168 thiE	28 4	60 9	225	thiamine phosphate pyrophosphorylase
2235	5735	2151039	2152118	1080	gp SC6E10_1	Streptomyces coelicolor A3(2) SC6E10.01	34 0	64 1	376	oxidoreductase
2236	5736	2152135	2152329	195	sp THIS_ECOLI	Escherichia coli K12 thiS	37 1	74 2	62	thiamine biosynthetic enzyme thiS (thiG1) protein
2237	5737	2152334	2153113	780	sp THIG_ECOLI	Escherichia coli K12 thiG	48 2	76 9	251	thiamine biosynthetic enzyme thiG protein
2238	5738	2153058	2154191	1134	prf 2417383A	Emericella nidulans cnxF	30 2	56 8	437	molybdopterin biosynthesis protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
2239	5739	2156733	2154460	2274	sp TEX_BORPE	Bordetella pertussis TOHAMA I tex	56.6	78.7	776	transcriptional accessory protein
2240	5740	2157721	2156747	975	pir A36940	Bacillus subtilis 168 degA	27.0	65.3	334	sporulation-specific degradation regulator protein
2241	5741	2159181	2157754	1428	pir B72105	Chlamydophila pneumoniae CWLC29 ybhI	45.8	78.3	456	dicarboxylase translocator
2242	5742	2159237	2159019	219	prf 2108268A	Spinacia oleracea chloroplast	40.0	80.0	65	2-oxoglutarate/malate translocator
2243	5743	2160537	2159287	1251	sp PCAB_PSEPU	Pseudomonas putida pcaB	39.1	66.3	350	3-carboxy-cis,cis-muconate cycloisomerase
2244	5744	2160670	2160768	99						
2245	5745	2161503	2161111	393						
2246	5745	2162196	2161507	690						
2247	5747	2163014	2162196	819	sp TRMD_ECOLI	Escherichia coli K12 trmD	34.8	64.8	273	tRNA (guanine-N1)-methyltransferase
2248	5748	2163098	2163745	648	gp SCF81_27	Streptomyces coelicolor A3(2) SCF81.27	30.5	57.6	210	hypothetical protein
2249	5749	2164260	2163748	513	sp RIMM_MYCLE	Mycobacterium leprae MLCB250.34 rimM	52.3	72.1	172	16S rRNA processing protein
2250	5750	2164390	2164737	348	pir B71881	Helicobacter pylori J99 jhp0839	29.0	66.7	69	hypothetical protein
2251	5751	2165309	2164815	495	pir C47154	Bacillus subtilis 168 rpsP	47.0	79.5	83	30S ribosomal protein S16
2252	5752	2165523	2166098	576	pir T14151	Mus musculus inv	32.1	61.7	196	inversin
2253	5753	2166990	2166124	867	prf 2512328G	Streptococcus agalactiae cylB	26.6	69.1	256	ABC transporter
2254	5754	2167865	2166990	876	prf 2220349C	Pyrococcus horikoshii OT3 mtrA	35.5	63.8	318	ABC transporter
2255	5755	2169584	2167944	1641	sp SR54_BACSU	Bacillus subtilis 168 ffh	58.7	78.2	559	signal recognition particle protein
2256	5756	2170425	2171058	633						
2257	5757	2171715	2172131	417						
2258	5758	2172203	2172877	669						
2259	5759	2175283	2173759	1530	sp FTSY_ECOLI	Escherichia coli K12 ftsY	37.0	66.1	505	cell division protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2260	5760	2176046	2175888	159						
2261	5761	2176402	2177103	702						
2262	5762	2179502	2176110	3393	sp AMYH_YEAST	Saccharomyces cerevisiae S288C YIR019C sta1	22 4	46 2	1144	glucan 1,4 alpha glucosidase or glucoamylase S1/S2 precursor
2263	5763	2180918	2181880	963						
2264	5764	2183092	2179628	3465	sp Y06B_MYCTU	Mycobacterium tuberculosis H37Rv Rv2922c smc	48 3	72 6	1206	chromosome segregation protein
2265	5765	2183391	2183110	282	sp ACYP_MYCTU	Mycobacterium tuberculosis H37Rv RV2922 1C	51.1	73 9	92	acylphosphatase
2266	5766	2185258	2183405	1854						
2267	5767	2185208	2185351	858	sp YFER_ECOLI	Escherichia coli K12 yfeR	23 9	60 0	305	transcriptional regulator
2268	5768	2186299	2187129	831	pir S72748	Mycobacterium leprae M_CL581 28c	39 3	73 5	257	hypothetical membrane protein
2269	5769	2187160	2187342	183						
2270	5770	2187679	2187233	447						
2271	5771	2188306	2187692	615	gp DNINTREG_3	Dichelobacter nodosus gep	46 8	76 6	188	cation efflux system protein
2272	5772	2189170	2188313	858	sp FPG_ECOLI	Escherichia coli K12 mutM or fpg	36 1	66 7	285	formamidopyrimidine-DNA glycosylase
2273	5773	2189906	2189166	741	pir B69693	Bacillus subtilis 168 rncS	40 3	76 5	221	ribonuclease III
2274	5774	2190439	2189906	534	sp Y06F_MYCTU	Mycobacterium tuberculosis H37Rv Rv2926c	35 8	62 5	176	hypothetical protein
2275	5775	2191328	2190540	789	sp Y06G_MYCTU	Mycobacterium tuberculosis H37Rv Rv2927c	50 0	76 9	238	hypothetical protein
2276	5776	2191522	2193165	1644	prf 2104260G	Streptomyces verticillus	28 3	55 6	559	transport protein
2277	5777	2193165	2194694	1530	sp CYDC_ECOLI	Escherichia coli K12 cydC	26 6	58 8	541	ABC transporter
2278	5778	2196883	2198004	1122	gp SC9C7_2	Streptomyces coelicolor A3(2) SC9C7 02	35 3	62 6	388	hypothetical protein
2279	5779	2198447	2198007	441						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2280	5780	2198475	2199758	1284	pir A72322	Thermotoga maritima MSB8 TM0896	21.0	43.7	405	hypothetical protein
2281	5781	2199808	2201070	1263	sp HIPO_CAMJE	Campylobacter jejuni ATCC 43431 hipO	32.9	64.3	353	peptidase
2282	5782	2201408	2201073	336	pir S38197	Arabidops s thaliana SUC1	27.1	51.9	133	sucrose transport protein
2283	5783	2201584	2201450	135						
2284	5784	2201869	2201594	276						
2285	5785	2204541	2201902	2550	prf 2513410A	Thermococcus litoralis malP	36.1	67.4	814	maltodextrin phosphorylase / glycogen phosphorylase
2286	5786	2205490	2204591	900	sp YFIE_BACSU	Bacillus subtilis 168 yfiE	33.9	66.4	295	hypothetical protein
2287	5787	2208249	2207302	948	sp LGT_STAAU	Staphylococcus aureus FDA 485 lgt	31.4	65.5	264	prolipoprotein diacylglyceryl transferase
2288	5788	2209167	2208367	801	sp TRPG_EMENI	Emericella nidulans trpC	29.6	62.1	169	indole-3-glycerol-phosphate synthase / anthranilate synthase component II
2289	5789	2209888	2209232	657	pir H70556	Mycobacterium tuberculosis H37Rv Rv1610	29.4	58.8	228	hypothetical membrane protein
2290	5790	2210273	2209920	354	sp HIS3_RHOSH	Rhodobacter sphaeroides ATCC 17023 hisI	52.8	79.8	89	phosphoribosyl-AMP cyclohydrolase
2291	5791	2211046	2210273	774	sp HIS6_CORG	Corynebacterium glutamicum AS019 hisF	97.3	97.7	258	cyclase
2292	5792	2211875	2211051	825	prf 2419176B	Corynebacterium glutamicum AS019 impA	94.0	94.0	241	inositol monophosphate phosphatase
2293	5793	2212619	2211882	738	gp AF051846_1	Corynebacterium glutamicum AS019 hisA	95.9	97.6	245	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase
2294	5794	2213273	2212641	633	gp AF060558_1	Corynebacterium glutamicum AS019 hisH	86.7	92.4	210	glutamine amidotransferase
2295	5795	2215086	2214321	1266	sp CMLR_STRLI	Streptomyces lividans 66 cmlR	25.6	54.0	402	chloramphenicol resistance protein or transmembrane transport protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2296	5796	2215863	2215639	225						
2297	5797	2216474	2215869	606	sp HIS7_STRCO	Streptomyces coelicolor A3(2) hisB	52 5	81 8	198	imidazoleglycerol phosphate dehydratase
2298	5798	2217591	2216494	1098	sp HIS8_STRCO	Streptomyces coelicolor A3(2) hisC	57 2	79 3	362	histidinol-phosphate aminotransferase
2299	5799	2218025	2217600	1326	sp H SX_MYCSM	Mycobacterium smegmatis ATCC 607 h sD	63 8	85.7	439	histidinol dehydrogenase
2300	5800	2219159	2220358	1200	gp SPBC215 13	Schizosaccharomyces pombe SPBC215.13	27 2	54.4	342	serine rich secreted protein
2301	5801	2221109	2220459	651						
2302	5802	2221611	2221919	309						
2303	5803	2221828	2221187	642	pir 2321269A	Leishmania donovani SAcP-1	29 4	59 7	211	histidine secretory acid phosphatase
2304	5804	2221959	2222518	561	pir RPECR1	Escherichia coli plasmid RP1 tetR	28 9	60 8	204	tet repressor protein
2305	5805	2222528	2225035	2508	pir 2307203B	Sulfolobus acidocaldarius treX	47 4	75 5	722	glycogen debranching enzyme
2306	5806	2225149	2225949	801	pir E70572	Mycobacterium tuberculosis H37Rv Rv2622	50 0	76 0	258	hypothetical protein
2307	5807	2225763	2225990	774	gp SC2G5_27	Streptomyces coelicolor A3(2) SC2G5 27c gp	29 9	55 2	268	oxidoreductase
2308	5808	2227779	2226769	1011	pir 2503399A	Sinorhizobium meliloti idhA	35 0	60 9	343	myo-inositol 2-dehydrogenase
2309	5809	2227906	2228901	996	sp GALR_ECOLI	Escherichia coli K12 galR	30 4	64 4	329	galactitol utilization operon repressor
2310	5810	2229896	2229099	798	sp FHUC_BACSU	Bacillus subtilis 168 fhuC	32 9	68 3	246	ferrichrome transport ATP binding protein or ferrichrome ABC transporter
2311	5811	2230937	2229900	1038	pir 2423441E	Vibrio cholerae hutC	36 8	71.1	332	hemin permease
2312	5812	2231294	2230947	348	pir G70046	Bacillus subtilis 168 yvrC	30 1	68 0	103	iron-binding protein
2313	5813	2231932	2231339	594	pir G70046	Bacillus subtilis 168 yvrC	34 6	67 6	182	iron binding protein
2314	5814	2232455	2232016	441	sp YTFH_ECOLI	Escherichia coli K12 ytfH	38 1	73 5	113	hypothetical protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2315	5815	2232928	2234070	1143	gp SCI8_12	Streptomyces coelicolor A3(2) SCI8.12	23.4	50.1	355	DNA polymerase III epsilon chain
2316	5816	2234158	2234763	606						
2317	5817	2234852	2237284	2433	pir S65769	Arthrobacter sp. Q36 treY	42.0	68.6	814	maltooligosyl trehalose synthase
2318	5818	2237331	2238353	1023	gp AE002006_4	Deinococcus radiodurans DR1631	27.6	52.8	322	hypothetical protein
2319	5819	2239092	2238694	399						
2320	5820	2240042	2239845	198						
2321	5821	2240246	2240058	189						
2322	5822	2240553	2239508	1056						
2323	5823	2240551	2241724	1044	sp LXA1_PHOLU	Photorhabdus luminescens ATCC 29999 luxA	20.5	54.4	375	alkanal monooxygenase alpha chain
2324	5824	2242115	2241738	378	gp SC7H2_5	Streptomyces coelicolor A3(2) SC7H2.05	58.3	79.2	120	hypothetical protein
2325	5825	2242369	2242129	231						
2326	5826	2243035	2244819	1785	pir S65770	Arthrobacter sp. Q36 treZ	46.3	72.4	568	maltooligosyltrehalose trehalohydrolase
2327	5827	2243013	2242393	651	sp YVYE_BACSU	Bacillus subtilis 168	36.5	72.4	214	hypothetical protein
2328	5828	2246171	2244864	1308	sp THD1_CORGL	Corynebacterium glutamicum ATCC 13032 ilvA	99.3	99.3	436	threonine dehydratase
2329	5829	2246386	2246892	507						
2330	5830	2246450	2246295	156						
2331	5831	2248208	2247006	1203	pir S57636	Catharanthus roseus metE	22.7	49.6	415	Corynebacterium glutamicum AS019
2332	5832	2251939	2248358	3582	prf 2508371A	Streptomyces coelicolor A3(2) dnaE	53.3	80.5	1183	DNA polymerase III
2333	5833	2252017	2252356	340	sp RARD_ECOLI	Escherichia coli K12 rarD	37.6	73.8	279	chloramphenicol sensitive protein
2334	5834	2253192	2253659	468	sp HISJ_CAMJE	Campylobacter jejuni DZ72 hisJ	21.5	55.7	149	histidine-binding protein precursor
2335	5835	2253725	2254642	918	pir D69548	Archaeoglobus fulgidus AF2388	22.7	64.7	198	hypothetical membrane protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2336	5836	2255558	2254683	876	sp G339_BACSU	Bacillus subtilis 168 ydaD	48.2	80.0	280	short chain dehydrogenase or general stress protein
2337	5837	2257024	2255738	1287	sp DCDA_PSEAE	Pseudomonas aeruginosa lysA	22 9	47 6	445	diaminopimelate (DAP) decarboxylase
2338	5838	2259312	2258362	951	sp CYSV_ALCEU	Alcaligenes eutrophus CH34 cysM	32.8	64 3	314	cysteine synthase
2339	5839	2259999	2259421	579						
2340	5840	2260931	2260002	930	sp RLUD_ECOLI	Escherichia coli K12 rluD	36.5	61 0	326	ribosomal large subunit pseudouridine synthase D
2341	5841	2261467	2260934	534	sp LSPA_PSEFL	Pseudomonas fluorescens NCIB 10585 lspA	33 8	61 7	154	lipoprotein signal peptidase
2342	5842	2261688	2263689	1002						
2343	5843	2262850	2264499	1650	pir S67863	Streptomyces antibioticus oleB	36 4	64 0	550	oleandomycin resistance protein
2344	5844	2264996	2265298	303						
2345	5845	2265108	2266509	600	prf2422382P	Rhodococcus erythropolis orf17	36 7	57 6	158	hypothetical protein
2346	5846	2265420	2266394	975	sp ASPG_BACLI	Bacillus licheniformis	31.2	62 0	321	L-asparaginase
2347	5847	2268297	2266897	1401	sp DINP_ECOLI	Escherichia coli K12 dinP	31.8	60 7	371	DNA-damage-inducible protein P
2348	5848	2269245	2268388	858	sp YBIF_ECOLI	Escherichia coli K12 ybiF	31 5	61 5	286	hypothetical membrane protein
2349	5849	2270261	2269260	1002	gp SCF51_6	Streptomyces coelicolor A3(2) SCF51.06	44.3	73 ·	334	transcriptional regulator
2350	5850	2270304	2270435	132						
2351	5851	2270884	2270258	627	gp SCF51_5	Streptomyces coelicolor A3(2) SCF51.05	42 0	67 0	212	hypothetical protein
2352	5852	2274149	2272998	1152	sp SYIC_YEAST	Saccharomyces cerevisiae A364A YBL076C ILS1	38 5	65 4	1006	isoleucyl-tRNA synthetase
2353	5853	2274688	2274473	216						
2354	5854	2275861	2274767	1095						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
2355	5855	2276637	2276353	285	pir F70578	Mycobacterium tuberculosis H37Rv Rv2146c	46.3	73.2	82	hypothetical membrane protein
2356	5856	2277336	2276881	456	gp BLFTS7_6	Brevibacterium lactofermentum orf6	99.3	99.3	152	hypothetical protein (putative YAK 1 protein)
2357	5857	2278078	2277416	663	sp YFZ1_CORGL	Corynebacterium glutamicum	97.7	99.6	221	hypothetical protein
2358	5858	2278859	2278122	738	prf 2420425C	Brevibacterium lactofermentum yfih	99.2	100.0	246	hypothetical protein
2359	5859	2279155	2278640	486	GP AB023808_1	Mus musculus P4(21)n	39.0	51.0	117	hypothetical protein
2360	5860	2280215	2278890	1326	sp FTSZ_BRLLA	Brevibacterium lactofermentum ftsZ	98.6	98.6	442	cell division protein
2361	5861	2281135	2280470	666	gsp W70502	Corynebacterium glutamicum ftsQ	99.6	100.0	222	cell division initiation protein or cell division protein
2362	5862	2282623	2281166	1458	gp AB015023_1	Corynebacterium glutamicum murC	99.4	99.8	486	UDP-N acetylmuramate- alanine ligase
2363	5863	2283779	2282661	1119	gp BLA242646_3	Brevibacterium lactofermentum ATCC 13869 murG	98.9	99.5	372	UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine pyrophosphoryl-undecaprenol N-acetylglucosamine
2364	5864	2285431	2283792	1650	gp BLA242646_2	Brevibacterium lactofermentum ATCC 13869 ftsW	99.4	99.6	490	cell division protein
2365	5865	2285904	2285437	468	gp BLA242646_1	Brevibacterium lactofermentum ATCC 13869 murD	99.1	99.1	110	UDP-N-acetylmuramoylalanine-D-glutamate ligase
2366	5866	2286272	2286655	384						
2367	5867	2286492	2286831	333						
2368	5868	2287959	2286852	1098	sp MRAY_ECOLI	Escherichia coli K12 mraY	38.6	63.8	365	phospho-n-acetylmuramoyl-pentapeptide
2369	5869	2289510	2287969	1542	sp MURF_ECOLI	Escherichia coli K12 murF	35.0	64.2	494	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate-D-alanyl-D-alanyl ligase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2370	5870	2291073	2289523	1551	sp MURE_BACSU	Bacillus subtilis 168 murE	37.7	67.6	491	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate-D-alanyl-D-alanyl ligase
2371	5871	2291197	2290973	225	GSP Y33117	Brevibacterium lactofermentum ORF2 pbp	100.0	100.0	57	penicillin binding protein
2372	5872	2293164	2291212	1953	pir S54872	Pseudomonas aeruginosa pbpB	28.2	58.8	650	penicillin-binding protein
2373	5873	2294117	2293323	795						
2374	5874	2295127	2294117	1011	pir A70581	Mycobacterium tuberculosis H37Rv Rv2165c	55.1	79.3	323	hypothetical protein
2375	5875	2295804	2295376	429	gp MLCB268_11	Mycobacterium leprae MLCB268.11c	72.0	88.8	143	hypothetical membrane protein
2376	5876	2296898	2296512	387	pir C70935	Mycobacterium tuberculosis H37Rv Rv2169c	39.4	69.3	137	hypothetical protein
2377	5877	2297653	2297231	423						
2378	5878	2297866	2298438	573	gp MLCB268_13	Mycobacterium leprae MLCB268.13	36.3	65.3	190	hypothetical protein
2379	5879	2299428	2298451	978	sp METF_STRLI	Streptomyces lividans 1326 metF	42.6	70.6	303	5,10-methylenetetrahydrofolate reductase
2380	5880	2299524	2300636	1113	pir S32168	Myxococcus xanthus DK1050 ORF1	30.1	62.0	329	dimethylallyltranstransferase
2381	5881	2300706	2302175	1470	gp MLCB268_16	Mycobacterium leprae MLCB268.17	35.7	69.6	484	hypothetical membrane protein
2382	5882	2302179	2302685	507						
2383	5883	2302619	2302981	360	pir A70936	Mycobacterium tuberculosis H37Rv Rv2175c	43.2	68.8	125	hypothetical protein
2384	5884	2302933	2304980	2148	gp AB019394_1	Streptomyces coelicolor A3(2) pkaF	34.2	62.4	684	eukaryotic-type protein kinase
2385	5885	2303690	2303040	651						
2386	5886	2304983	2306218	1236	gp MLCB268_21	Mycobacterium leprae MLCB268.23	30.7	58.4	411	hypothetical membrane protein

Table 1 (continued)

SEQ NO. (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2387	5887	2306314	2307621	1308	pir G70936	Mycobacterium tuberculosis H37Rv Rv2181	30 4	62 0	434	hypothetical membrane protein
2388	5888	2309082	2307697	1386	gp AF260581_2	Amycolatopsis mediterranei	66 9	87 9	462	3-deoxy-D-arabino-heptulosonate-7-phosphate synthase
2389	5889	2309676	2309173	504	gp MLCB268 20	Mycobacterium leprae MLCB268.21c	58 4	77 7	166	hypothetical protein
2390	5890	2309835	2312252	2418	pir G70936	Mycobacterium tuberculosis H37Rv Rv2181	35.1	64 5	428	hypothetical membrane protein
2391	5891	2312360	2313808	1449	sp CSP1_CORGL	Corynebacterium glutamicum (Brevibacterium flavum) ATCC 17965 csp1	28 2	57 1	440	major secreted protein PS1 protein precursor
2392	5892	2313833	2314036	204						
2393	5893	2314092	2313916	177						
2394	5894	2315423	2314236	1188	gp AF096280_3	Corynebacterium glutamicum ATCC 13032	100.0	100.0	249	hypothetical membrane protein
2395	5895	2316412	2315678	735	gp AF096280_2	Corynebacterium glutamicum ATCC 13032	100.0	100 0	245	acyltransferase
2396	5896	2318775	2317633	1143	gp SC6G10_5	Streptomyces coelicolor A3(2) SC6G10.05c	50 1	75.7	383	glycosyl transferase
2397	5897	2319850	2318804	1047	sp P60_LISIV	Listeria ivanovii iap	26.4	60 8	296	protein P60 precursor (invasion-associated-protein)
2398	5898	2320594	2319968	627	sp P60_LISGR	Listeria grayi iap	33 0	61.3	191	protein P60 precursor (invasion-associated-protein)
2399	5899	2323073	2321472	1602	prf 2503462K	Heliobacillus mobilis petB	34 3	64.7	201	ubiquinol-cytochrome c reductase cytochrome b subunit
2400	5900	2323759	2323088	672	gp AF107888_1	Streptomyces lividans qcrA	37 9	57 1	203	ubiquinol-cytochrome c reductase iron-sulfur subunit (Rieske [eFe-2S] iron-sulfur protein cyoB
2401	5901	2325195	2324311	885	sp Y005_MYCTU	Mycobacterium tuberculosis H37Rv Rv2194 qcrC	58 6	83 1	278	ubiquinol-cytochrome c reductase cytochrome c

Table 1 (continued)

SEQ NO. (DNA)	SEQ NO. (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2402	5902	2325887	2325273	615	sp COX3_SYNVU	Synechococcus vulcanus	36.7	70.7	188	cytochrome c oxidase subunit III
2403	5903	2326273	2326121	153						
2404	5904	2326900	2326472	429	sp Y00A_MYCTU	Mycobacterium tuberculosis H37Rv Rv2199c	38.6	71.0	145	hypothetical membrane protein
2405	5905	2327997	2326921	1077	sp COX2_RHOSH	Rhodobacter sphaeroides ctaC	28.7	53.9	317	cytochrome c oxidase subunit II
2406	5906	2328516	2330435	1920	gp AB029550_1	Corynebacterium glutamicum KY9611 ltsA	99.7	99.8	640	glutamine-dependent amidotransferase or asparagine synthetase (lysozyme insensitivity protein)
2407	5907	2330927	2330586	342	gp AB029550_2	Corynebacterium glutamicum KY9611 orf1	100.0	100.0	114	hypothetical protein
2408	5908	2331200	2331967	768	gp MLCB22_2	Mycobacterium leprae MLCB22.07	35.0	60.2	246	hypothetical membrane protein
2409	5909	2331974	2332495	522	pir S52220	Rhodobacter capsulatus cobP	43.0	64.0	172	cobinamide kinase
2410	5910	2332512	2333600	1089	sp COBU_PSEDE	Pseudomonas denitrificans cobU	37.8	66.9	341	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase
2411	5911	2333615	2334535	921	sp COBV_PSEDE	Pseudomonas denitrificans cobV	25.3	49.8	305	cobalamin (5'-phosphate) synthase
2412	5912	2334717	2334481	237						
2413	5913	2335741	2335028	714	prf 2414335A	Streptomyces clavuligerus car	38.6	68.5	241	clavulanate 9 aldehyde reductase
2414	5914	2337051	2335915	1137	sp ILVE_MYCTU	Mus musculus BCAT1	40.1	70.3	364	branched-chain amino acid aminotransferase
2415	5915	2337235	2338734	1500	gp PPU010261_1	Pseudomonas putida ATCC 12633 pepA	36.3	65.9	493	leucyl aminopeptidase
2416	5916	2339140	2338748	393	prf 2110282A	Saccharopolyspora erythraea ORF1	40.2	67.0	97	hypothetical protein
2417	5917	2339269	2341293	2025	gp AF047034_2	Streptomyces sequlensis pdhB	48.9	68.5	691	dihydrolipoamide acetyltransferase
2418	5918	2340804	2339440	1365						
2419	5919	2341412	2342164	753	gp AB020975_1	Arabidopsis thaliana	36.7	65.7	210	lipoyltransferase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2420	5920	2342304	2343347	1044	sp LIPA_PELCA	Pelobacter carbinolicus GRA BD 1 lipA	44.6	70.9	285	lipoic acid synthetase
2421	5921	2343479	2344258	780	sp Y00U_MYCTU	Mycobacterium tuberculosis H37Rv Rv2219	45.5	76.7	257	hypothetical membrane protein
2422	5922	2344431	2346047	1617	sp YIDE_ECOLI	Escherich a coli K12 yidE	32.9	67.8	559	hypothetical membrane protein
2423	5923	2347491	2346289	1203	gp AF189147_1	Corynebacterium glutamicum ATCC 13032 tnp	100.0	100.0	401	transposase (ISCg2)
2424	5924	2347505	2347804	300						
2425	5925	2348549	2348078	471	gp SC5F7_34	Streptomyces coelicolor A3(2) SC5F7.04c	41.4	63.7	157	hypothetical membrane protein
2426	5926	2350620	2350408	213						
2427	5927	2351022	2351996	975			31.0	44.0	145	mutator mutT domain protein
2428	5928	2351310	2350912	399	pir B72308	Thermotoga maritima MSB8 TM1010	36.7	65.6	128	hypothetical protein
2429	5929	2351909	2351310	600						
2430	5930	2351980	2352828	849	sp LUXA_VIBHA	Vibrio harveyi luxA	25.0	60.9	220	alkanal monooxygenase alpha chain (bacterial luciferase alpha chain)
2431	5931	2352813	2353225	393	pir A72404	Thermotoga maritima MSB8 TM0215	40.5	73.0	111	protein synthesis inhibitor (translation initiation inhibitor)
2432	5932	2355156	2355398	243						
2433	5933	2355440	2355180	261						
2434	5934	2355521	2356843	1323	prf 2203345H	Escherichia coli hpaX	21.9	53.4	433	4-hydroxyphenylacetate permease
2435	5935	2356794	2357354	561	gp SCGD3_10	Streptomyces coelicolor A3(2) SCGD3.10c	42.4	72.8	158	transmembrane transport protein
2436	5936	2357264	2357707	444	gp SCGD3_10	Streptomyces coelicolor A3(2) SCGD3.10c	31.4	66.1	118	transmembrane transport protein
2437	5937	2357484	2357290	195						
2438	5938	2357726	2358130	405						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (aa)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (aa)	Function
2439	5939	2358095	2358153	543						
2440	5940	2359416	2358772	645	sp HMUO_CORDI	Corynebacterium diphtheriae C7 hmuO	57.9	78.0	214	heme oxygenase
2441	5941	2362748	2359614	3135	gp SCY17736_4	Streptomyces coelicolor A3(2) glnE	43.4	67.0	809	glutamate-ammonia-ligase adenylyltransferase
2442	5942	2364155	2362818	1338	sp GLNA_THEMA	Thermotoga maritima MSB8 glnA	43.5	73.0	441	glutamine synthetase
2443	5943	2364352	2365455	1104	gp SCE9_39	Streptomyces coelicolor A3(2) SCE9.39c	26.8	54.1	392	hypothetical protein
2444	5944	2365587	2367413	1827	sp Y017_MYCTU	Mycobacterium tuberculosis H37Rv Rv2226	33.4	58.2	601	hypothetical protein
2445	5945	2367662	2367473	190	gp SCC75A_11	Streptomyces coelicolor A3(2) SCC75A.11c	38.9	55.6	54	hypothetical protein
2446	5946	2367791	2369083	1293	sp GAL1_HUMAN	Homo sapiens galK1	24.9	53.7	374	galactokinase
2447	5947	2370381	2369116	1266	gp AF174645_1	Brucella abortus vacB	27.1	54.5	358	virulence-associated protein
2448	5948	2370423	2370908	486						
2449	5949	2372557	2371412	1146	sp Y019_MYCTU	Mycobacterium tuberculosis H37Rv Rv2228c	54.7	75.1	382	bifunctional protein (ribonuclease H and phosphoglycerate mutase)
2450	5950	2372661	2373389	729						
2451	5951	2373289	2372573	717	sp Y01A_MYCTU	Mycobacterium tuberculosis H37Rv Rv2229c	26.5	58.6	249	hypothetical protein
2452	5952	2374462	2373323	1140	sp Y01B_MYCTU	Mycobacterium tuberculosis H37Rv Rv2230c	49.2	76.2	378	hypothetical protein
2453	5953	2374644	2375197	554	sp GPH_ECOLI	Escherichia coli K12 gph	26.0	54.4	204	phosphoglycolate phosphatase
2454	5954	2375214	2375684	471	sp PTFA_STRCO	Streptomyces coelicolor A3(2) SCQ11.04c ptpA	46.2	63.5	156	low molecular weight protein-tyrosine-phosphatase
2455	5955	2375767	2376720	954	sp Y01G_MYCTU	Mycobacterium tuberculosis H37Rv Rv2235	40.9	65.5	281	hypothetical protein
2456	5956	2377396	2376698	393	sp Y12_BURCE	Burkholderia cepacia	32.6	56.6	129	insertion element (IS402)

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
2457	5957	2377726	2377484	243						
2458	5958	2377899	2378276	378	gp SC8F4_22	Streptomyces coelicolor A3(2) SC8F4.22c	30.4	57.8	135	transcriptional regulator
2459	5959	2378292	2378489	198						
2460	5960	2379312	2378884	429	sp Y01K_MYCTU	Mycobacterium tuberculosis H37Rv Rv2239c	55.2	77.6	134	hypothetical protein
2461	5961	2379426	2379770	345						
2462	5962	2380033	2382744	2712	gp AF047034_4	Streptomyces seoulensis pdhA	55.9	78.9	910	pyruvate dehydrogenase component
2463	5963	2382240	2380765	1476						
2464	5964	2383615	2382827	789	sp GLNQ_ECOLI	Escherichia coli K12 glnQ	33.7	62.8	261	ABC transporter or glutamine transport ATP-binding protein
2465	5965	2384464	2385426	963						
2466	5966	2384509	2383622	888	sp RBSC_BACSU	Bacillus subtilis 168 rbsC	25.4	58.7	283	ribose transport system permease protein
2467	5967	2385447	2384509	939	pir H71693	Rickettsia prowazekii Madrid E RP367	26.2	62.9	286	hypothetical protein
2468	5968	2385771	2386580	810	sp CBPA_DICDI	Dictyostelium discoideum AX2 cbpA	41.6	55.2	125	calcium binding protein
2469	5969	2386284	2385913	372						
2470	5970	2387027	2388014	1014	gp SC6G4_24	Streptomyces coelicolor A3(2) SC6G4.24	29.6	55.7	352	lipase or hydrolase
2471	5971	2387667	2387957	291	sp ACP_MYXXA	Myxococcus xanthus ATCC 25232 acpP	42.7	80.0	75	acyl carier protein
2472	5972	2387997	2388821	825	sp NAGD_ECOLI	Escherichia coli K12 nagD	43.9	75.5	253	N-acetylglucosamine-6-phosphate deacetylase
2473	5973	2388838	2389869	1032	gp AE001968_4	Deinococcus radiodurans DR1192	33.6	65.7	289	hypothetical protein
2474	5974	2390904	2390434	471						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2475	5975	2392008	2391184	825	gp SC4A7_8	Streptomyces coelicolor A3(2) SC4A7.08	52.4	75.3	271	hypothetical protein
2476	5976	2392566	2392075	492						
2477	5977	2393349	2392579	771						
2478	5978	2393425	2393970	546						
2479	5979	2394437	2393973	465						
2480	5980	2394594	2394935	342						
2481	5981	2395204	2396763	1560	sp PPBD_BACSU	Bacillus subtilis 168 phoD	34.2	64.7	530	alkaline phosphatase D precursor
2482	5982	2395986	2395273	714						
2483	5983	2397264	2399099	1836	gp SCI51_17	Streptomyces coelicolor A3(2) SCI51.17	44.4	73.1	594	hypothetical protein
2484	5984	2399158	2399397	240	pir G70661	Mycobacterium tuberculosis H37Rv Rv2342	41.2	72.1	68	hypothetical protein
2485	5985	2400342	2399668	675						
2486	5986	2401303	2399405	1899	prf 2413330B	Mycobacterium smegmatis dnaG	59.1	82.9	633	DNA primase
2487	5987	2401373	2401834	462	gp XXU39467_1	Streptomyces aureofaciens BMK	49.0	67.4	98	ribonuclease Sa
2488	5988	2401838	2402080	243						
2489	5989	2403165	2402530	636						
2490	5990	2404012	2402144	1869	gp AF058788_1	Mycobacterium smegmatis mc2155 glmS	59.4	82.2	636	L-glutamine D-fructose 6-phosphate amidotransferase
2491	5991	2404523	2404846	324						
2492	5992	2405671	2406822	1152						
2493	5993	2406258	2404987	1272	prf 2413330A	Mycobacterium smegmatis dgt	54.6	76.3	414	deoxyguanosinetriphosphate triphosphohydrolase
2494	5994	2406936	2406262	675	gp NMA1Z2491_23 5	Neisseria meningitidis NMA0251	30.4	59.7	171	hypothetical protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2495	5995	2408993	2409029	2037	pir B70662	Mycobacterium tuberculosis H37Rv Rv2345	31.1	63.6	692	hypothetical protein
2496	5996	2410264	2409779	486	gp AE003565_26	Drosophila melanogaster CG10592	24.6	54.4	138	hypothetical protein
2497	5997	2410861	2410280	582						
2498	5998	2412338	2410956	1383	pir S58522	Thermus aquaticus HB8	46.1	69.9	508	glycyl-tRNA synthetase
2499	5999	2412580	2412948	369	pir E70585	Mycobacterium tuberculosis H37Rv Rv2358 furB	49.4	73.0	89	bacterial regulatory protein, arsR family
2500	6000	2412992	2413423	432	sp FUR_ECOLI	Escherichia coli K12 fur	34.9	70.5	132	ferric uptake regulation protein
2501	6001	2413568	2415118	1551	pir A70539	Mycobacterium tuberculosis H37Rv Rv1128c	24.8	46.7	529	hypothetical protein (conserved in C glutamicum?)
2502	6002	2416089	2416298	792	gp AF162938_1	Streptomyces coelicolor A3(2) h3u	40.6	67.0	224	hypothetical membrane protein
2503	6003	2417099	2416371	729	sp UPPS_MICLU	Micrococcus luteus B-P 26 uppS	43.4	71.2	233	undecaprenyl diphosphate synthase
2504	6004	2417947	2417222	726	pir A70586	Mycobacterium tuberculosis H37Rv Rv2362c	45.7	74.3	245	hypothetical protein
2505	6005	2418883	2417969	915	gp AF072811_1	Streptococcus pneumoniae era	39.5	70.3	296	Era-like GTP-binding protein
2506	6006	2420309	2418990	1320	sp Y1DE_MYCTU	Mycobacterium tuberculosis H37Rv Rv2366	52.8	82.4	432	hypothetical membrane protein
2507	6007	2420900	2420313	588	sp YN67_MYCTU	Mycobacterium tuberculosis H37Rv Rv2367c	65.0	86.0	157	hypothetical protein
2508	6008	2420973	2421236	264	GSP Y75650	Neisseria meningitidis	45.0	50.0	85	Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics
2509	6009	2421949	2420900	1050	sp PHOL_MYCTU	Mycobacterium tuberculosis H37Rv Rv2368c phoH	61.1	84.6	344	phosphate starvation inducible protein
2510	6010	2422697	2421975	723	gp SCC77_19	Streptomyces coelicolor A3(2) SCC77.19c	44.0	75.4	248	hypothetical protein
2511	6011	2422850	2423791	942						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2512	6012	2423845	2422700	1146	prf 2421342B	Streptomyces albus dnaJ2	47.1	77 4	380	heat shock protein dnaJ
2513	6013	2424937	2423915	1023	prf 2421342A	Streptomyces albus hrcA	48.2	79 6	334	heat-inducible transcriptional repressor (groEL repressor)
2514	6014	2425954	2424905	990	prf 2318256A	Bacillus stearothermophilus hemN	33 1	64 1	320	oxygen-independent coproporphyrinogen III oxidase
2515	6015	2426181	2426699	519	sp AGA1_YEAST	Saccharomyces cerevisiae YNR044W AGA1	36 6	64 9	134	agglutinin attachment subunit precursor
2516	6016	2427468	2426776	693						
2517	6017	2428184	2427807	378						
2518	6018	2430028	2428184	1845	gp SC6G10_4	Streptomyces coelicolor A3(2) SC6G10 04	48 0	75 1	611	long-chain-fatty-acid- CoA ligase
2519	6019	2430296	2432413	2118	sp MALQ_ECOLI	Escherichia coli K12 malQ	28 3	55 4	738	4-alpha-glucanotransferase
2520	6020	2432509	2434370	1863	gp AB005752_1	Lactobacillus brevis plasmid horA	29 5	64 4	604	ABC transporter, Hop-Resistance protein
2521	6021	2433868	2433614	255	GSP Y74827	Neisseria gonorrhoeae	44 0	51 0	68	Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics
2522	6022	2434207	2433875	333	GSP Y74829	Neisseria meningitidis	47 0	53 0	107	polypeptides predicted to be useful antigens for vaccines and diagnostics
2523	6023	2434619	2434440	180						
2524	6024	2434776	2434573	204						
2525	6025	2436838	2434805	2034	sp DCP_SALTY	Salmonella typhimurium dcp	40 3	68 3	690	peptidyl-dipeptidase
2526	6026	2436871	2438049	1179	gp AF064523_1	Anisopteromalus calandrae	24 1	45.7	453	carboxylesterase
2527	6027	2438113	2439906	1794	pir G70983	Mycobacterium tuberculosis H37Rv Rv0126	65 2	84 9	594	glycosyl hydrolase or trehalose synthase
2528	6028	2439906	2440994	1089	pir H70983	Mycobacterium tuberculosis H37Rv Rv0127	32 1	58 8	449	hypothetical protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (aa)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (aa)	Function
2529	6029	2441589	2441005	585	pir T07979	Chlamydomonas reinhardtii ipi1	31.8	57.7	189	isopentenyl-diphosphate Delta-isomerase
2530	6030	2441669	2441890	222						
2531	6031	2442355	2442792	438						
2532	6032	2443356	2441602	1755						
2533	6033	2444015	2443356	660						
2534	6034	2444551	2444033	519						
2535	6035	2444735	2445709	975	gp CORCSLYS_1	Corynebacterium glutamicum ATCC 13032 aecD	99.4	100.0	325	beta C-S lyase (degradation of aminoethylcysteine)
2536	6036	2445719	2446993	1278	sp BRNQ_CORGL	Corynebacterium glutamicum ATCC 13032 brnQ	99.8	100.0	426	branched-chain amino acid transport system carrier protein (isoleucine uptake)
2537	6037	2447021	2447998	978	sp LUXA_VIBHA	Vibrio harveyi luxA	21.6	49.0	343	alkanal monooxygenase alpha chain
2538	6038	2450844	2450323	522						
2539	6039	2451785	2450859	927	gp AF155772_2	Sinorhizobium meliloti mdcF	25.9	60.5	324	malonate transporter
2540	6040	2454637	2451794	2844	sp GLCD_ECOLI	Escherichia coli K12 glcD	27.7	55.1	483	glycolate oxidase subunit
2541	6041	2454725	2455435	711	sp YDFH_ECOLI	Escherichia coli K12 ydfH	25.6	65.0	203	transcriptional regulator
2542	6042	2455733	2455452	282						
2543	6043	2457079	2455720	1347	sp YGIK_SALTY	Salmonella typhimurium ygiK	22.5	57.6	467	hypothetical protein
2544	6044	2457759	2457337	423						
2545	6045	2457863	2459371	1509	sp HBPA_HAEIN	Haemophilus influenzae Rd HI0853 hbpA	27.5	55.5	546	heme-binding protein A precursor (hemin-binding lipoprotein)
2546	6046	2459371	2460336	966	sp APPB_BACSU	Bacillus subtilis 168 appB	40.0	73.3	315	oligopeptide ABC transporter (permease)
2547	6047	2460340	2461167	828	sp DPPC_ECOLI	Escherichia coli K12 dppC	43.2	74.5	271	dipeptide transport system permease protein
2548	6048	2461163	2462599	1437	prf 2306258MR	Escherichia coli K12 oppD	37.4	66.4	372	oligopeptide transport ATP-binding protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2549	6049	2462049	2461543	507	PIR G72536	Aeropyrum pernix K1 APE1580	35 0	44 0	106	hypothetical protein
2550	6050	2463150	2462602	549	pir D70367	Aquifex aeolicus VF5 aq_768	29 3	58 0	157	hypothetical protein
2551	6051	2463241	2464143	903	prf 2514301A	Rhizobium etli rbsK	41 0	65 0	300	ribose kinase
2552	6052	2464344	2465768	1425	gp SCM2_16	Streptomyces coelicolor A3(2) SCM2 16c	39 9	64 6	466	hypothetical membrane protein
2553	6053	2465767	2465465	303						
2554	6054	2467009	2466038	972	sp NTCI_HUMAN	Homo sapiens	31 3	61 6	284	sodium dependent transporter or odium Bile acid symporter family
2555	6055	2467077	2467922	846	gp AF135243_1	Chlamydomonas reinhardtii	28 5	51 2	295	apospory-associated protein C
2556	6056	2470313	2470678	366						
2557	6057	2472250	2472819	570	sp THIX_CORGL	Corynebacterium glutamicum ATCC 13032 thiX	100 0	100 0	133	thiamine biosynthesis protein x
2558	6058	2473460	2472893	588	sp VG66_BPMD	Mycobacteriophage D29 66	42 6	65 5	197	hypothetical protein
2559	6059	2473653	2475542	1890	sp BETP_CORGL	Corynebacterium glutamicum ATCC 13032 betP	39 8	71 7	601	glycine betaine transporter
2560	6060	2476497	2477492	996						
2561	6061	2477644	2479251	1608						
2562	6062	2479379	2479762	384						
2563	6063	2481208	2479898	1311	prf 2320266C	Rhodobacter capsulatus dctM	34 6	71 9	448	large integral C4-dicarboxylate membrane transport protein
2564	6064	2481692	2481213	480	gp AF186091_1	Klebsiella pneumoniae dctQ	33 9	73 7	118	small integral C4-dicarboxylate membrane transport protein
2565	6065	2482480	2481734	747	sp DCTP_RHOCA	Rhodobacter capsulatus B10 dctP	28 2	59 0	227	C4-dicarboxylate-binding periplasmic protein precursor
2566	6066	2483845	2484087	243	PRF 1806416A	Lycopersicon esculentum (tomato)	63 0	73 0	46	extensin
2567	6067	2484392	2482548	1845	sp LEPA_BACSU	Bacillus subtilis 168 lepA	58 7	83 6	603	GTP-binding protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (aa)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (aa)	Function
2568	6068	2484661	2485269	609	pir H70683	Mycobacterium tuberculosis H37Rv Rv2405	41.6	69.7	185	hypothetical protein
2569	6069	2485473	2485733	261	sp RS20_ECOLI	Escherichia coli K12 rpsT	48.2	72.9	85	30S ribosomal protein S20
2570	6070	2486469	2485801	669	sp RHTC_ECOLI	Escherichia coli K12 rhtC	30.0	67.1	210	thrreonine efflux protein
2571	6071	2486881	2486477	405	gp SC6D7_25	Streptomyces coelicolor A3(2) SC6D7.25	61.2	80.6	129	ankyrin-like protein
2572	6072	2487884	2486910	975	pir H70684	Mycobacterium tuberculosis H37Rv Rv2413c	46.0	74.1	313	hypothetical protein
2573	6073	2489450	2487912	1539	sp CME3_BACSU	Bacillus subtilis 168 comEC	21.4	49.7	527	late competence operon required for DNA binding and uptake
2574	6074	2490154	2489573	582	sp CME1_BACSU	Bacillus subtilis 168 comEA	30.8	63.6	195	late competence operon required for DNA binding and uptake
2575	6075	2490911	2491732	822						
2576	6076	2491111	2490290	822	gp SCC123_7	Streptomyces coelicolor A3(2) SCC123.07c	34.8	66.3	273	hypothetical protein
2577	6077	2491858	2491151	708	pir F70685	Mycobacterium tuberculosis H37Rv Rv2419c	46.8	66.4	235	phosphoglycerate mutase
2578	6078	2492343	2491873	471	pir G70685	Mycobacterium tuberculosis H37Rv Rv2420c	55.6	86.3	117	hypothetical protein
2579	6079	2493178	2492501	678	gp SCC123_17	Streptomyces coelicolor A3(2) SCC123.17c	68.0	85.3	197	hypothetical protein
2580	6080	2494237	2493215	1023						
2581	6081	2495834	2494339	1296	sp PROA_CORGL	Corynebacterium glutamicum ATCC 17965 proA	99.1	99.8	432	gamma-glutamyl phosphate reductase or glutamate-5-semialdehyde dehydrogenase
2582	6082	2496607	2495696	912	sp YPRA_CORGL	Corynebacterium glutamicum ATCC 17965 unkdh	99.3	100.0	304	D-isomer specific 2-hydroxyacid dehydrogenase
2583	6083	2496803	2497513	711						
2584	6084	2499511	2498009	1503	gp D87915_1	Streptomyces coelicolor A3(2) obg	58.9	78.2	487	GTP-binding protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
2585	6085	2499783	2501669	1887	sp.PBUX_BACSU	Bacillus subtilis 168 pbuX	39.1	77.3	422	xanthine permease
2586	6086	2502577	2501735	843	pir.I40838	Corynebacterium sp. ATCC 31090	61.2	81.9	276	2,5-diketo-D-gluconic acid reductase
2587	6087	2502735	2503355	621						
2588	6088	2503870	2504265	396						
2589	6089	2504247	2503984	264	sp.RL27_STRGR	Streptomyces griseus IFO13189 rpmA	80.3	92.6	81	50S ribosomal protein L27
2590	6090	2504602	2504300	303	pir.2304263A	Streptomyces griseus IFO13189 obg	56.4	82.2	101	50S ribosomal protein L21
2591	6091	2507098	2504831	2268	sp.RNE_ECOLI	Escherichia coli K12 rne	30.1	56.6	886	ribonuclease E
2592	6092	2507115	2507663	549						
2593	6093	2507138	2507710	573						
2594	6094	2508094	2508840	747						
2595	6095	2508922	2509530	609	gp.SCF76_8	Streptomyces coelicolor A3(2) SCF76.08c	61.0	82.6	195	hypothetical protein
2596	6096	2510830	2509523	1308	pir.S43613	Corynebacterium glutamicum ATCC 31831	99.1	100.0	436	transposase (insertion sequence IS31831)
2597	6097	2511046	2511423	378	gp.SCF76_8	Streptomyces coelicolor A3(2) SCF76.08c	51.3	76.9	117	hypothetical protein
2598	6098	2511427	2511876	450	gp.SCF76_9	Streptomyces coelicolor A3(2) SCF76.09	37.8	67.8	143	hypothetical protein
2599	6099	2512356	2511949	408	gp.AF069544_1	Mycobacterium smegmatis ndk	70.9	89.6	134	nucleoside diphosphate kinase
2600	6100	2512768	2512409	360						
2601	6101	2512803	2513144	342	gp.AE002024_10	Deinococcus radiodurans R1 DR1844	34.8	67.4	92	hypothetical protein
2602	6102	2513618	2513154	465	pir.H70515	Mycobacterium tuberculosis H37Rv Rv1883c	36.6	64.3	112	hypothetical protein
2603	6103	2514114	2513692	423	pir.E70863	Mycobacterium tuberculosis H37Rv Rv2446c	33.9	68.6	118	hypothetical protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initia (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
2604	6104	2515487	2514114	1374	prf 2410252B	Streptomyces coelicolor A3(2) folC	55.4	79.6	451	folyl-polyglutamate synthetase
2605	6105	2515662	2516273	612						
2606	6106	2516243	2516956	714						
2607	6107	2517089	2517751	663						
2608	6108	2518336	2515637	2700	sp SYV_BACSU	Bacillus subtilis 168 balS	45.5	72.1	915	valyl-tRNA synthetase
2609	6109	2519972	2518398	1575	pir A38447	Bacillus subtilis 168 oppA	24.2	58.5	521	oligopeptide ABC transport system substrate-binding protein
2610	6110	2520209	2521660	1452	sp DNAK_BACSU	Bacillus subtilis 168 dnaK	26.2	54.9	508	heat shock protein dnaK
2611	6111	2522251	2521667	585	gp ECU89166_1	Eikenella corrodens ATCC 23824	42.9	71.2	170	lysine decarboxylase
2612	6112	2523248	2522265	984	sp MDH_THEFL	Thermus aquaticus ATCC 33923 mdh	56.4	76.5	319	malate dehydrogenase
2613	6113	2523561	2524337	777	gp SC4A10_33	Streptomyces coelicolor A3(2) SC4A10.33	24.6	56.5	207	transcriptional regulator
2614	6114	2524915	2524340	576	gp AF065442_1	Vibrio cholerae aphA	26.0	51.4	208	hypothetical protein
2615	6115	2525099	2526226	1128	prf 2513416F	Acinetobacter sp. vanA	39.5	68.6	357	vanillate demethylase (oxygenase)
2616	6116	2526233	2527207	975	gp FSU12290_2	Sphingomonas flava ATCC 39723 pcpD	32.8	59.2	338	pentachlorophenol 4-monooxygenase reductase
2617	6117	2527135	2528559	1425	prf 2513416G	Acinetobacter sp. vanK	40.8	76.8	444	transport protein
2618	6118	2529480	2528551	930	gp KPU95087_7	Klebsiella pneumoniae mdcF	28.0	58.4	286	malonate transporter
2619	6119	2530761	2529484	1278	prf 2303274A	Bacillus subtilis clpX	59.8	85.8	430	class-III heat-shock protein or ATP-dependent protease
2620	6120	2530991	2531076	1086	gp SCF55_28	Streptomyces coelicolor A3(2) SCF55.28c	45.6	73.0	366	hypothetical protein
2621	6121	2532601	2531969	633	gp AF109386_2	Streptomyces sp. 2065 pcaJ	63.3	85.7	210	succinyl CoA:3-oxoadipate CoA transferase beta subunit
2622	6122	2533252	2532694	750	gp AF109386_1	Streptomyces sp. 2065 pcaI	60.2	84.5	251	succinyl CoA:3-oxoadipate CoA transferase alpha subunit

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2623	6123	2533391	2534182	792	prf 2408324F	Rhodococcus opacus 1CP pcaR	58.2	82.5	251	protocatechuate catabolic protein
2624	6124	2534201	2535424	1224	prf 2411305D	Ralstonia eutropha bktB	44.8	71.9	406	beta ketothiolase
2625	6125	2535168	2534257	912						
2626	6126	2535430	2536182	753	prf 2408324E	Rhodococcus opacus pcaL	50.8	76.6	256	3-oxoadipate enol-lactone hydrolase and 4-carboxymuconolactone decarboxylase
2627	6127	2536196	2539256	2061	gp SCM1_10	Streptomyces coelicolor A3(2) SCM1.10	23.6	43.0	825	transcriptional regulator
2628	6128	2538613	2539249	366	prf 2408324F	Rhodococcus opacus pcaL	78.3	89.6	115	3-oxoadipate enol-lactone hydrolase and 4-carboxymuconolactone decarboxylase
2629	6129	2539553	2540230	678						
2630	6130	2539731	2538616	1116	prf 2408324D	Rhodococcus opacus pcaB	39.8	63.4	437	3-carboxy-cis,cis-muconate cycloisomerase
2631	6131	2540320	2539709	612	prf 2408324C	Rhodococcus opacus pcaG	49.5	70.6	214	protocatechuate dioxygenase alpha subunit
2632	6132	2541024	2540335	690	prf 2408324B	Rhodococcus opacus pcaH	74.7	91.2	217	protocatechuate dioxygenase beta subunit
2633	6133	2542350	2541187	1164	pir G70506	Mycobacterium tuberculosis H37Rv Rv0336	26.4	48.7	273	hypothetical protein
2634	6134	2542802	2542512	291	prf 2515333B	Mycobacterium tuberculosis catC	54.4	81.5	92	muconolactone isomerase
2635	6135	2543043	2543813	771						
2636	6136	2543936	2542818	1119	sp CATB_RHOOP	Rhodococcus opacus 1CP catB	60.8	84.7	372	muconate cycloisomerase
2637	6137	2544262	2544867	606						
2638	6138	2544876	2544022	855	prf 2503218A	Rhodococcus rhodochrous catA	72.3	88.4	285	catechol 1,2-dioxygenase
2639	6139	2545068	2544928	141						
2640	6140	2545315	2546784	1470	gp AF134348_1	Pseudomonas putida plasmid pDK1 xylX	62.2	85.6	437	toluate 1,2 dioxygenase subunit

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
2641	6141	2546827	2547318	492	gp AF134348_2	Pseudomonas putida plasmid pDK1 xylY	60.3	83.2	161	toluate 1,2 dioxygenase subunit
2642	6142	2547333	2548868	1536	gp AF134348_3	Pseudomonas putida plasmid pDK1 xylZ	51.5	81.0	342	toluate 1,2 dioxygenase subunit
2643	6143	2548868	2549695	828	gp AF134348_4	Pseudomonas putida plasmid pDK1 xylL	30.7	61.4	277	1,2-dihydroxycyclohexa-3,5-diene carboxylate dehydrogenase
2644	6144	2549771	2552455	2685	gp RFU95170_1	Rhodococcus erythropolis thcG	23.3	48.6	979	regulator of LuxR family with ATP-binding site
2645	6145	2553563	2553942	1380	sp PCAK_ACICA	Acinetobacter calcoaceticus pcaK	31.3	64.4	435	transmembrane transport protein or 4-hydroxybenzoate transporter
2646	6146	2554020	2555207	1242	sp BENE_ACICA	Acinetobacter calcoaceticus benE	29.9	66.2	388	benzoate membrane transport protein
2647	6147	2555940	2555317	624	gp AF071885_2	Streptomyces coelicolor M145 clpP2	69.5	88.3	197	ATP-dependent Clp protease proteolytic subunit 2
2648	6148	2556580	2555978	603	gp AF071885_1	Streptomyces coelicolor M145 clpP1	62.1	85.9	198	ATP-dependent Clp protease proteolytic subunit 1
2649	6149	2556599	2556749	150	gp SIS243537_4	Sulfolobus islandicus ORF154	42.9	71.4	42	hypothetical protein
2650	6150	2558106	2556760	1347	sp TIG_BACSU	Bacillus subtilis 168 tig	32.1	66.4	417	trigger factor (prolyl isomerase) (chaperone protein)
2651	6151	2558609	2559103	495	gp SCD25_17	Streptomyces coelicolor A3(2) SCD25.17	32.5	63.1	160	hypothetical protein
2652	6152	2559157	2560131	975	sp PBP4_NOCLA	Nocardia lactamdurans LC411 pbp	25.3	50.9	336	penicillin-binding protein
2653	6153	2560131	2560586	456	prf 2301342A	Mus musculus Moa1	27.8	58.3	115	hypothetical protein
2654	6154	2561115	2561363	249						
2655	6155	2561920	2561483	438	prf 2513302C	Corynebacterium striatum ORF1	54.2	73.2	142	transposase
2656	6156	2562093	2562242	150						
2657	6157	2562115	2561990	126	prf 2513302C	Corynebacterium striatum ORF1	57.1	82.9	35	hypothetical protein
2658	6158	2562341	2562078	264	prf 2513302C	Corynebacterium striatum ORF1	50.7	78.7	75	transposase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (aa)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (aa)	Function
2659	6159	2562776	2562387	390						
2660	6160	2562963	2563847	885						
2661	6161	2564402	2563933	471	sp LACB_STAAU	Staphylococcus aureus NCTC 8325-4 lacB	40 0	71 4	140	galactose-6-phosphate isomerase
2662	6162	2565245	2564550	696	sp YAMY_BACAD	Bacillus acidopullulyticus ORF2	26 2	58 1	248	hypothetical protein
2663	6163	2566231	2565623	609	pir A70866	Mycobacterium tuberculosis H37Rv Rv2466c	56 8	80 9	199	hypothetical protein
2664	6164	2566345	2568945	2601	sp AMPN_STRLI	Streptomyces lividans pepN	47 5	70 5	890	aminopeptidase N
2665	6165	2569211	2570293	1083	pir B70206	Borrelia burgdorferi BB0852	25 1	58 1	358	hypothetical protein
2666	6166	2571460	2570309	1152						
2667	6167	2571510	2572175	666						
2668	6168	2572193	2572348	156						
2669	6169	2572677	2572351	327	gp AF139916_3	Brevibacterium linens ATCC 9175 crtI	61 5	81 7	104	phytoene desaturase
2670	6170	2572977	2572807	171						
2671	6171	2573770	2573393	378						
2672	6172	2572864	2572959	1236	sp CRTJ_MYXXA	Myxococcus xanthus DK1050 carA2	31 2	63 8	381	phytoene dehydrogenase
2673	6173	2574718	2573843	876	sp CRTB_STRGR	Streptomyces griseus JA3933 crtB	31 4	58 6	290	phytoene synthase
2674	6174	2575898	2574780	1119	gp LMAJ9627_3	Listeria monocytogenes IltB	25 8	47 7	392	multidrug resistance transporter
2675	6175	2577213	2575981	1233						
2676	6176	2578872	2577232	1641	gp SYOATPBP_2	Synechococcus elongatus	41 3	71 6	538	ABC transporter ATP-binding protein
2677	6177	2579760	2578879	882	sp DPPC_BACFI	Bacillus firmus OF4 dppC	38 8	73 8	286	dipeptide transport system permease protein
2678	6178	2580707	2579769	939	pir S47696	Escherichia coli K12 nikB	33 2	62 0	316	*nickel transport* system permease protein
2679	6179	2582417	2580711	1707						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2680	6180	2582564	2584504	1941						
2681	6181	2584613	2585926	1314	sp ARGD_CORGL	Corynebacterium glutamicum ATCC 13032 argD	31.4	63.5	411	acetylornithine aminotransferase
2682	6182	2586180	2587763	1584	pir A70539	Mycobacterium tuberculosis H37Rv Rv1128c	25.1	47.9	482	hypothetical protein
2683	6183	2587976	2588722	747	sp YA20_MYCTU	Mycobacterium tuberculosis H37Rv Rv0364	49.1	79.4	218	hypothetical membrane protein
2684	6184	2589432	2588725	708	sp PHBB_CHRVI	Chromatium vinosum D phbB	28.1	60.0	235	acetoacetyl CoA reductase
2685	6185	2589565	2590302	738	pir A40046	Streptomyces coelicolor actII	26.7	55.0	240	transcriptional regulator, TetR family
2686	6186	2590697	2591137	441	GSP:1174375	Neisseria meningitidis	38.0	47.0	94	polypeptides predicted to be useful antigens for vaccines and diagnostics
2687	6187	2592365	2591574	792	gp AF106002_1	Pseudomonas putida GM73 ttg2A	31.1	65.1	238	ABC transporter ATP-binding protein
2688	6188	2592402	2592794	393	gp MLCB1610_9	Mycobacterium leprae MLCB1610.14c	53.2	77.0	126	globin
2689	6189	2592838	2593965	1128	sp CHRA_PSEAE	Pseudomonas aeruginosa Plasmid pUM505 chrA	27.3	60.4	396	chromate transport protein
2690	6190	2594534	2593968	567	pir A70867	Mycobacterium tuberculosis H37Rv Rv2474c	37.8	68.9	196	hypothetical protein
2691	6191	2595061	2594597	465	gp SC6D10_19	Streptomyces coelicolor A3(2) SC6D10.19c	36.2	61.4	127	hypothetical protein
2692	6192	2595808	2595188	621						
2693	6193	2595983	2595822	162	pir B72589	Aeropyrum pernix K1 APE1182	36.4	60.0	55	hypothetical protein
2694	6194	2597715	2596048	1668	sp YJJK_ECOLI	Escherichia coli K12 yjjK	52.8	79.6	563	ABC transporter ATP-binding protein
2695	6195	2598483	2597869	615	pir E70867	Mycobacterium tuberculosis H37Rv Rv2478c	31.4	62.2	172	hypothetical protein
2696	6196	2600764	2598662	2103	sp Y05L_MYCLE	Mycobacterium leprae o659	28.0	56.7	700	hypothetical membrane protein
2697	6197	2603461	2602879	1419	pir C69676	Bacillus subtilis phoB	28.0	52.6	536	alkaline phosphatase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (aa)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (aa)	Function
2698	6198	2604573	2605502	930						
2699	6199	2604583	2603945	639		Streptococcus mutans INGBRITT msmG	39.1	76.3	279	multiple sugar binding transport system permease protein
2700	6200	2605522	2604609	912	sp MSMG_STRMU					
2701	6201	2606369	2605527	843	sp MSMF_STRMU	Streptococcus mutans INGBRITT msmF	27.4	67.5	292	multiple sugar-binding transport system permease protein
2702	6202	2606444	2608117	1674						
2703	6203	2607889	2606561	1329	prf 2206392C	Thermoanaerobacterium thermosul amyE	28.8	63.2	462	maltose binding protein
2704	6204	2609426	2608185	1242						
2705	6205	2610639	2609513	1128	prf 2308356A	Streptomyces reticuli msiK	59.1	79.8	386	ABC transporter ATP binding protein (ABC-type sugar transport protein) or cellobiose/maltose transport protein
2706	6206	2611523	2611272	252						
2707	6207	2611531	2610848	684	prf 2317468A	Schizosaccharomyces pombe dpm1	37.7	72.7	154	dolichol phosphate mannose synthase
2708	6208	2612462	2613151	690						
2709	6209	2613712	2614500	789	prf 2516398E	Rhodococcus rhodochrous plasmid pRTL1 orf5	67.2	89.4	207	aldehyde dehydrogenase
2710	6210	2614649	2615410	762	prf 2513418A	Synechococcus sp PCC7942 cpmA	48.6	73.8	183	circadian phase modifier
2711	6211	2615451	2615795	345						
2712	6212	2617120	2615939	1182	pir A72312	Thermotoga maritima MSB8 TM0964	35.0	64.6	412	hypothetical membrane protein
2713	6213	2617246	2617995	750	sp GIP_ECOLI	Escherichia coli K12 gip	41.2	69.4	255	glyoxylate induced protein
2714	6214	2618072	2618869	798	pir E70761	Mycobacterium tuberculosis H37Rv Rv1544	40.0	57.0	258	ketoacyl reductase
2715	6215	2618882	2619538	657	sp ORN_ECOLI	Escherichia coli K12 orn	48.0	78.8	179	oligoribonuclease

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2716	6216	2620728	2619541	1188	prf 2409378A	Salmonella enterica iroD	26.0	50.9	454	ferric enterochelin esterase
2717	6217	2622181	2620973	1209	pir C70870	Mycobacterium tuberculosis H37Rv Rv2516c lppS	48.5	71.9	398	lipoprotein
2718	6218	2622961	2623605	645						
2719	6219	2623770	2623621	150						
2720	6220	2623893	2624048	246						
2721	6221	2625358	2624051	1308	gp SCU53587_1	Corynebacterium glutamicum ATCC 21086	99.5	99.8	436	transposase (IS1207)
2722	6222	2625600	2625806	207						
2723	6223	2626447	2625809	639						
2724	6224	2627924	2628376	453	gp AF085239_1	Salmonella typhimurium KP1001 cytR	32.8	63.4	131	transcriptional regulator
2725	6225	2628121	2626493	1629	sp GLSK_RAT	Rattus norvegicus SPRAGUE-DAWLEY KIDNEY	35.2	69.3	358	glutaminase
2726	6226	2628376	2628852	477	pir A36940	Bacillus subtilis 168 degA	42.3	72.2	97	sporulation-specific degradation regulator protein
2727	6227	2628878	2628324	555						
2728	6228	2628926	2630479	1554	sp UXAC_ECOLI	Escherichia coli K12 uxaC	29.0	60.9	335	uronate isomerase
2729	6229	2630636	2631136	501						
2730	6230	2631270	2632466	1197	prf 1814452C	Zea diploperennis perennial teosinte	32.0	45.0	291	hypothetical protein
2731	6231	2632543	2633100	558	prf 2324444A	Mycobacterium avium pncA	48.1	74.6	185	pyrazinamidase/nicotinamidase
2732	6232	2633418	2633146	273	pir E70870	Mycobacterium tuberculosis H37Rv Rv2520c	42.7	80.0	75	hypothetical protein
2733	6233	2633600	2634064	465	sp BCP_ECOLI	Escherichia coli K12 bcp	46.8	73.8	141	bacterioferritin comigratory protein
2734	6234	2634116	2634751	636	gp SCI11_1	Streptomyces coelicolor A3(2) SCI11.01c	32.5	61.4	114	bacterial regulatory protein, tetR family

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (aa)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (aa)	Function
2735	6235	2635151	2634747	405	gp BAY15081_1	Corynebacterium ammoniagenes ATCC 6871 ppt1	56 6	75 9	145	phosphopantetheine protein transferase
2736	6236	2636589	2635165	1425	gp AF237667_1	Corynebacterium glutamicum lmrB	52 4	85 6	473	lincomycin resistance protein
2737	6237	2636845	2637168	324	pir S76537	Synechocystis sp PCC6803	30 1	54 0	113	hypothetical membrane protein
2738	6238	2637653	2637240	414						
2739	6239	2647627	2638649	8979	pir S72047	Corynebacterium ammoniagenes fas	62 3	83 6	3029	fatty-acid synthase
2740	6240	2649416	2648235	1182	gp SC4A7 14	Streptomyces coelicolor A3(2) SC4A7 14	25 3	55 2	404	hypothetical protein
2741	6241	2649550	2650164	615	pir D70716	Mycobacterium tuberculosis H37Rv Rv0950c	40 4	60 9	230	peptidase
2742	6242	2650441	2650902	462	sp Y077_MYCT	Mycobacterium tuberculosis H37Rv Rv1343c	40 2	67 9	112	hypothetical membrane protein
2743	6243	2650986	2651339	354	sp Y076_MYCLE	Mycobacterium leprae B1549_F2_59	37 2	69 0	113	hypothetical membrane protein
2744	6244	2652037	2651420	618	sp Y03Q_MYCTU	Mycobacterium tuberculosis H37Rv Rv1341	55 0	76 7	202	hypothetical protein
2745	6245	2652801	2652067	735	sp RNPH_PSEAE	Pseudomonas aeruginosa ATCC 15692 rph	60 2	81 4	236	ribonuclease PH
2746	6246	2653254	2653009	246						
2747	6247	2654018	2653326	693						
2748	6248	2654660	2654079	582						
2749	6249	2656236	2654875	1362	sp Y029_MYCTU	Mycobacterium tuberculosis H37Rv SC8A6 09c	29 0	58 2	428	hypothetical membrane protein
2750	6250	2656452	2656985	534	gp AF121000_8	Corynebacterium glutamicum 22243 R-plasmid pAG1 tnpB	92 1	97 2	175	transposase (IS1628)
2751	6251	2657633	2656974	660						
2752	6252	2658500	2657736	765	sp Y030_MYCLE	Mycobacterium leprae als	46 0	74 4	250	arylsulfatase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2753	6253	2659457	2658606	852	prf 2516259A	Corynebacterium glutamicum ATCC 13869 murI	99.3	99.3	284	D-glutamate racemase
2754	6254	2659496	2660131	636						
2755	6255	2660638	2660147	492	gp SCE22_22	Streptomyces coelicolor A3(2) SCE22.22	44.2	70.8	147	bacterial regulatory protein, marR family
2756	6256	2661417	2660671	747	sp Y03M_MYCTU	Mycobacterium tuberculosis H37Rv Rv1337	38.2	69.3	225	hypothetical membrane protein
2757	6257	2661555	2662455	891						
2758	6258	2662375	2661417	959	pir A47039	Flavobacterium sp nylC	30.2	58.3	321	endo-type 6-aminohexanoate oligomer hydrolase
2759	6259	2662867	2662331	537	sp Y03H_MYCTU	Mycobacterium tuberculosis H37Rv Rv1332	35.0	58.5	200	hypothetical protein
2760	6260	2663182	2662883	300	sp Y03G_MYCTU	Mycobacterium tuberculosis H37Rv Rv1331	57.1	77.1	105	hypothetical protein
2761	6261	2663437	2664060	624						
2762	6262	2664060	2665397	1338	sp Y03F_MYCTU	Mycobacterium tuberculosis H37Rv Rv1330c	61.2	80.8	428	hypothetical protein
2763	6263	2665687	2665992	306						
2764	6264	2666115	2667854	1740	prf 1816252A	Escherichia coli dinG	25.2	53.3	647	ATP-dependent helicase
2765	6265	2668760	2667870	891	sp Y0A8_MYCTU	Mycobacterium tuberculosis H37Rv Rv2560	29.7	60.1	313	hypothetical membrane protein
2766	6266	2669561	2668839	723	pir T34684	Streptomyces coelicolor A3(2) SC1B5.06c	39.0	52.0	222	hypothetical protein
2767	6267	2670573	2669557	1017	sp SERB_ECOLI	Escherichia coli K12 serB	38.7	61.0	310	phosphoserine phosphatase
2768	6268	2671126	2672721	1596						
2769	6269	2672805	2671063	1743	pir D45335	Mycobacterium tuberculosis H37Rv Rv3043c	46.8	74.4	575	cytochrome c oxidase chain I
2770	6270	2672950	2673255	306						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2771	6271	2674339	2673338	1002	gp AF112536_1	Corynebacterium glutamicum ATCC 13032 nrdF	99 7	99 7	334	ribonucleotide reductase beta chain
2772	6272	2674804	2675289	486	sp FTNA_ECOLI	Escherichia coli K12 ftnA	31 5	64 2	159	ferritin
2773	6273	2675491	2676240	750	gp SCA32WHIH_4	Streptomyces coelicolor A3(2) whiH	32 8	60 2	256	sporulation transcription factor
2774	6274	2676802	2676242	660	pir I40339	Corynebacterium glutamicum ATCC 13869 dtxR	27 6	60 4	225	iron dependent repressor of diptheria toxin repressor
2775	6275	2676910	2677277	438	sp TIR2_YEAST	Saccharomyces cerevisiae YPH148 YOR010C TIR2	24 2	62 1	124	cold shock protein TIR2 precursor
2776	6276	2677193	2676918	276	pir C69281	Archaeoglobus fulgidus AF0251	50 0	86 0	50	hypothetical membrane protein
2777	6277	2679598	2677478	2121	gp AF112535_3	Corynebacterium glutamicum ATCC 13032 nrdE	99 9	100 0	707	ribonucleotide reductase alpha chain
2778	6278	2680470	2680784	315	SP RL36_RICPR	Ricketts a prowazekii	58 0	79 0	41	50S ribosomal protein L36
2779	6279	2681363	2681223	141	sp NADE_BACSU	Bacillus subtilis 168 nadE	55 6	78 1	279	NH3-dependent NAD(+) synthetase
2780	6280	2681546	2682376	831						
2781	6281	2681556	2681464	93						
2782	6282	2683119	2683616	498						
2783	6283	2683125	2682379	747	pir S76790	Synechocystis sp PCC6803 slr1563	30 7	56 4	257	hypothetical protein
2784	6284	2683418	2683131	288	pir G70922	Mycobacterium tuberculosis H37Rv Rv3129	41 7	68 8	96	hypothetical protein
2785	6285	2683646	2683627	1020	sp ADH2_BACST	Bacillus stearothermophilus DSM 2334 adh	26 1	52 8	337	alcohol dehydrogenase
2786	6286	2684919	2683989	1371	sp MMGE_BACSU	Bacillus subtilis 168 mmgE	27 0	56 0	459	Bacillus subtilis mmg (for mother cell metabolic genes)
2787	6287	2686315	2687148	834	pir T05174	Arabidopsis thaliana T6K22 50	33 8	66 2	284	hypothetical protein
2788	6288	2688240	2687449	792						
2789	6289	2690050	2688389	1662	sp PGMU_ECOLI	Escherichia coli K12 pgm	61 7	80 6	556	phosphoglucomutase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2790	6290	2690150	2690437	288	pir F70650	Mycobacterium tuberculosis H37Rv Rv3069	41.7	64.3	84	hypothetical membrane protein
2791	6291	2690437	2690760	324	pir D71843	Helicobacter pylori J99 jhp1146	25.4	61.5	122	hypothetical membrane protein
2792	6292	2690773	2691564	792	sp YCSI_BACSU	Bacillus subtilis 168 ycsI	51.2	79.1	254	hypothetical protein
2793	6293	2691689	2693053	1365	gp AF126281_1	Rhodococcus erythropolis	24.2	48.6	496	transposase (IS1676)
2794	6294	2693299	2694918	1620	sp CSP1_CORGL	Corynebacterium glutamicum (Brevibacterium flavum) ATCC 17965 csp1	24.8	49.6	355	major secreted protein PS1 protein precursor
2795	6295	2694926	2695279	354						
2796	6296	2695554	2695718	165						
2797	6297	2695766	2695320	447						
2798	6298	2695812	2697212	1401	gp AF126281_1	Rhodococcus erythropolis	24.6	46.6	500	transposase (IS1676)
2799	6299	2698150	2697383	768						
2800	6300	2699531	2698194	1338	sp GLTT_BACCA	Bacillus subtilis 168	30.8	66.2	438	proton/sodium-glutamate symport protein
2801	6301	2700920	2701612	693						
2802	6302	2702466	2699926	2541	gp SCE25_30	Streptomyces coelicolor A3(2) SCE25.30	33.0	69.0	873	ABC transporter
2803	6303	2702466	2703356	891						
2804	6304	2703194	2702487	708	gp SAU18641_2	Staphylococcus aureus	45.4	79.8	218	ABC transporter ATP-binding protein
2805	6305	2704314	2704586	273	PIR F81516	Chlamydophila pneumoniae AR39 CP0987	60.0	67.0	84	hypothetical protein
2806	6306	2704835	2704975	141	PIR F81737	Chlamydia muridarum Nigg TC0129	71.0	75.0	42	hypothetical protein
2807	6307	2709878	2710555	678						
2808	6308	2710837	2711508	672	prf 2509388L	Streptomyces collinus Tu 1892 ansG	28.1	54.1	196	oxidoreductase or dehydrogenase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2809	6309	2711850	2712374	525	sp Y089_MYCTU	Mycobacterium tuberculosis H37Rv Rv0089	25.9	51.2	205	methyltransferase
2810	6310	2713151	2713453	273	GSP Y35814	Chlamydia pneumoniae	61.0	66.0	84	hypothetical protein
2811	6311	2713702	2713842	141	PIR F81737	Chlamydia muridarum Nigg TC0129	71.0	75.0	42	hypothetical protein
2812	6312	2718187	2717993	195						
2813	6313	2719689	2718436	1254	sp MURA_ACICA	Acinetobacter calcoaceticus NCIB 8250 murA	44.8	75.3	417	UDP-N acetylglucosamine 1-carboxyvinyltransferase
2814	6314	2719750	2720319	570	sp Y02Y_MYCTU	Mycobacterium tuberculosis H37Rv Rv1314c	66.3	84.2	190	hypothetical protein
2815	6315	2721227	2720385	843	gp SC2G5_15	Streptomyces coelicolor A3(2) SC2G5.15c	45.9	69.0	281	transcriptional regulator
2816	6316	2721702	2721295	408						
2817	6317	2721934	2722857	924	sp CYSK_BACSU	Bacillus subtilis 168 cysK	57.1	84.6	305	cysteine synthase
2818	6318	2723064	2723609	546	prf 2417357C	Azotobacter vinelandii cysE?	61.1	79.7	172	O-acetylserine synthase
2819	6319	2724057	2723770	288	gp AE002024_10	Deinococcus radiodurans R1 DR1844	36.1	65.1	83	hypothetical protein
2820	6320	2725359	2724478	882	sp SUCD_COXBU	Coxiella burnetii Nine Mile Ph I sucD	52.9	79.4	291	succinyl CoA synthetase alpha chain
2821	6321	2725619	2725843	225	PIR F72706	Aeropyrum pernix K1 APE1069	42.0	43.0	75	hypothetical protein
2822	6322	2726577	2725384	1194	sp SUCC_BACSU	Bacillus subtilis 168 sucC	39.8	73.0	400	succinyl-CoA synthetase beta chain
2823	6323	2727145	2726786	360						
2824	6324	2728133	2727399	735	gp AF058302_5	Streptomyces roseofulvus fmE	38.5	71.8	213	frenolicin gene E product
2825	6325	2729025	2728207	819						
2826	6326	2730916	2729378	1539	sp CAT1_CLOKL	Clostridium kluyveri cat1 cat1	47.9	77.8	501	succinyl-CoA coenzyme A transferase
2827	6327	2731376	2732518	1143	sp NIR3_AZOBR	Azospirillum brasilense ATCC 29145 ntrC	38.6	68.5	321	transcriptional regulator

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
2829	6328	2732230	2731424	807						
2829	6329	2732836	2733367	732	pir E70810	Mycobacterium tuberculosis H37Rv Rv0821c phoY-2	46.5	81.7	213	phosphate transport system regulatory protein
2830	6330	2734351	2733455	897	pir S68595	Pseudomonas aeruginosa pstB	58.8	82.8	255	phosphate-specific transport component
2831	6331	2735184	2734264	921	gp MTPSTA1_1	Mycobacterium tuberculosis H37Rv Rv0830 pstA1	51.4	82.2	292	phosphate ABC transport system permease protein
2832	6332	2736215	2735202	1014	pir A70584	Mycobacterium tuberculosis H37Rv Rv0829 pstC2	50.2	78.5	325	phosphate ABC transport system permease protein
2833	6333	2737538	2736414	1125	pir H70583	Mycobacterium tuberculosis H37Rv phoS2	40.0	56.0	369	phosphate-binding protein S-3 precursor
2834	6334	2738711	2737835	876	gp SCD84_18	Streptomyces coelicolor A3(2) SCD84.18c	34.3	60.0	315	acetyltransferase
2835	6335	2738771	2739553	783						
2836	6336	2740650	2739556	1095	sp BMRU_BACSU	Bacillus subtilis 168 bmrU	24.7	55.2	344	hypothetical protein
2837	6337	2740670	2741356	687	pir E70809	Mycobacterium tuberculosis H37Rv Rv0813c	44.9	74.2	225	hypothetical protein
2838	6338	2742577	2741636	942	gp AF193846_1	Solanum tuberosum BCAT2	28.6	56.0	259	branched-chain amino acid aminotransferase
2839	6339	2742685	2743785	1101	gp AB003158_6	Corynebacterium ammoniagenes ATCC 6872 ORF4	58.5	79.0	352	hypothetical protein
2840	6340	2741019	2744222	213	pir B70809	Mycobacterium tuberculosis H37Rv Rv0810c	58.6	81.0	58	hypothetical protein
2841	6341	2745954	2744881	1074	gp AB003158_5	Corynebacterium ammoniagenes ATCC 6872 purM	81.0	94.2	347	5'-phosphoribosyl-5-aminoimidazole synthetase
2842	6342	2747564	2746083	1482	gp AB003158_4	Corynebacterium ammoniagenes ATCC 6872 purF	70.3	89.0	482	amidophosphoribosyl transferase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2843	6343	2748057	2747683	375	pir H70536	Mycobacterium tuberculosis H37Rv Rv0807	57 3	75 8	124	hypothetical protein
2844	6344	2748095	2749111	1017	gp AB003158_2 ORF2	Corynebacterium ammoniagenes ATCC 6872	75 9	94 0	315	hypothetical protein
2845	6345	2749092	2749162	741	gp AB003158_1	Corynebacterium ammoniagenes ATCC 6872 ORF1	67 7	87 1	217	hypothetical membrane protein
2846	6346	2751918	2752103	186	GP SSU18930_21 4	Sulfolobus solfataricus	64 0	71 0	42	hypothetical protein
2847	6347	2752312	2750627	2386	gp AB003162_3	Corynebacterium ammoniagenes ATCC 6872 purL	77 6	89 5	763	5' phosphoribosyl N formylglycinamidine synthetase
2848	6348	2752402	2753121	720						
2849	6349	2752995	2752327	669	gp AB003162_2	Corynebacterium ammoniagenes ATCC 6872 purQ	80 3	93 3	223	5'-phosphoribosyl-N-formylglycinamidine synthetase
2850	6350	2753237	2752995	243	gp AB003162_1	Corynebacterium ammoniagenes ATCC 6872 purorf	81 0	93 7	79	hypothetical protein
2851	6351	2753298	2753819	522						
2852	6352	2753804	2753328	477	prf 2420329A	Lactococcus lactis gpo	46 2	77 9	158	gluthatione peroxidase
2853	6353	2753992	2756739	2748	prf 2216389A	Aeromonas hydrophila JMP636 nucH	28 0	51 5	965	extracellular nuclease
2854	6354	2756851	2757126	276						
2855	6355	2757815	2757129	687	pir C70709	Mycobacterium tuberculosis H37Rv Rv0784	37 4	68 7	211	hypothetical protein
2856	6356	2759200	2757863	1338	sp DCTA_SALTY	Salmonella typhimurium LT2 dctA	49 0	81 6	414	C4 dicarboxylate transporter
2857	6357	2761649	2759532	2118	prf 2408266A	Pseudomonas sp WO24 dapb1	41 8	70 6	697	dipeptidyl aminopeptidase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2859	6358	2762452	2761829	624						
2859	6359	2762875	2761785	891	gp AB003161_3	Corynebacterium ammoniagenes ATCC 6872 purC	70.1	89.1	294	5'-phosphoribosyl-4-N-succinocarboxamide-5-amino imidazole synthetase
2860	6360	2764931	2763504	1428	gp AB003161_2	Corynebacterium ammoniagenes ATCC 6872 purB	85.3	95.0	477	adenylosuccino lyase
2861	6361	2766135	2764978	1158	sp AAT_SULSO	Sulfolobus solfataricus ATCC 49255	28.1	62.3	395	aspartate aminotransferase
2862	6362	2767420	2766158	1263	gp AB003161_1	Corynebacterium ammoniagenes ATCC 6872 purD	71.1	86.4	425	5'-phosphoribosylglycinamide synthetase
2863	6363	2767580	2767993	414	sp YHIT_MYCLE	Mycobacterium leprae U296a	53.7	80.2	136	histidine triad (HIT) family protein
2864	6364	2768137	2767703	435						
2865	6365	2769095	2768343	753	pir S62195	Methanosarcina barkeri orf3	26.8	56.4	243	hypothetical protein
2866	6366	2770511	2769156	1356	sp DTPT_LACLA	Lactococcus lactis subsp lactis dipT	30.1	67.6	469	di-/tripeptide transpoter
2867	6367	2770714	2771982	1269	sp BIOA_CORGL	Corynebacterium glutamicum (Brevibacterium flavum) MJ233 bioA	95.7	98.8	423	adenosylmethionine-8-amino-7-oxononanoate aminotransferase or 7,8-diaminopelargonic acid aminotransferase
2868	6368	2771989	2772660	672	sp BIOD_CORGL	Corynebacterium glutamicum (Brevibacterium flavum) MJ233 bioD	98.7	99.6	224	dethiobiotin synthetase
2869	6369	2774098	2772644	1455	gp AF049873_3	Lactococcus lactis M71plasmid pND306	31.3	70.5	335	two-component system sensor histidine kinase
2870	6370	2774814	2774110	705	prf 2222216A	Thermologa maritima drrA	42.0	72.7	231	two-component system regulatory protein
2871	6371	2775689	2774937	753	sp TIPA_STRLI	Streptomyces lividans tipA	37.4	69.5	249	transcriptional activator
2872	6372	2776879	2775740	1140	prf 2419350A	Arthrobacter sp DK-38	30.9	53.9	382	metal-activated pyridoxal enzyme or low specificity D-Thr aldolase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2873	6373	2778504	2776768	1737	gp ECOPOXB8G_1	Escherichia coli K12 poxB	46.3	75.8	574	pyruvate oxidase
2874	6374	2778065	2780446	1482	prf 2212334B	Staphylococcus aureus plasmid pSK23 qacB	33.3	68.9	504	multidrug efflux protein
2875	6375	2780429	2780959	531	sp YCDC_ECOLI	Escherichia coli K12 ycdC	30.4	68.5	92	transcriptional regulator
2876	6376	2780996	2782315	1320	pir D70551	Mycobacterium tuberculosis H37Rv Rv2508c	45.6	78.4	421	hypothetical membrane protein
2877	6377	2784481	2782340	2142						
2878	6378	2785615	2784656	960	gp AF096929_2	Rhodococcus erythropolis SQ1 kstD1	34.3	62.1	303	3-ketosteroid dehydrogenase
2879	6379	2786355	2785651	705	sp ALSR_BACSU	Bacillus subtilis 168 alsR	37.1	69.0	232	transcriptional regulator, LysR family
2880	6380	2787782	2788594	813	pir C70982	Mycobacterium tuberculosis H37Rv Rv3298c lpqC	28.4	52.9	278	hypothetical protein
2881	6381	2789399	2788587	813	pir C69862	Bacillus subtilis 168 ykrA	26.7	55.6	288	hypothetical protein
2882	6382	2789935	2789477	459						
2883	6383	2790152	2790550	399	pir A45264	Oryctolagus cuniculus kidney cortex rBAT	28.6	50.7	140	hypothetical protein
2884	6384	2790946	2792448	1503	pir B70798	Mycobacterium tuberculosis H37Rv Rv3737	36.0	64.0	464	hypothetical membrane protein
2885	6385	2792531	2792857	327	pir S41307	Streptomyces griseus hrdB	32.3	50.3	155	transcription initiation factor sigma
2886	6386	2792873	2794327	1455	sp TPS1_SCHPO	Schizosaccharomyces pombe tps1	38.8	66.7	487	trehalose-6-phosphate synthase
2887	6387	2794300	2794812	513						
2888	6388	2794870	2795637	768	sp OTSB_ECOLI	Escherichia coli K12 otsB	27.4	57.6	245	trehalose-phosphatase
2889	6389	2796749	2795676	1074	sp CCPA_BACME	Bacillus megaterium ccpA	24.7	60.2	344	glucose-resistance amylase regulator
2890	6390	2796865	2797806	942	sp ZNUA_HAEIN	Haemophilus influenzae Rd HI0119 znuA	22.4	46.7	353	high-affinity zinc uptake system protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
2891	6391	2797820	2798509	690	gp:AF121672_2	Staphylococcus aureus 8325-4 mreA	31.4	53.2	223	ABC transporter
2892	6392	2798837	2799391	555	pir:B70507	Mycobacterium tuberculosis H37Rv Rv2060	60.0	87.4	135	hypothetical membrane protein
2893	6393	2799535	2801034	1500	pir:A69426	Archaeoglobus fulgidus	23.4	52.5	303	transposase (ISA0963.5)
2894	6394	2801113	2801313	201						
2895	6395	2803246	2801558	1689	gp:AF096929_2	Rhodococcus erythropolis SQ1 kstD1	32.1	62.0	561	3-ketosteroid dehydrogenase
2896	6396	2803996	2803250	747						
2897	6397	2804691	2804074	618	pir:B72359	Thermotoga maritima MSB8 bplA	34.3	56.4	204	lipopolysaccharide biosynthesis protein or oxidoreductase or dehydrogenase
2898	6398	2805110	2804676	435	sp:MI2D_BACSU	Bacillus subtilis 168 idh or iolG	35.2	59.5	128	dehydrogenase or myo-inositol 2-dehydrogenase
2899	6399	2805967	2805113	855	sp:SHIA_ECOLI	Escherichia coli K12 shiA	30.5	67.5	292	shikimate transport protein
2900	6400	2806441	2806016	426	sp:SHIA_ECOLI	Escherichia coli K12 shiA	43.1	80.8	130	shikimate transport protein
2901	6401	2807252	2806599	654	gp:SC5A7_19	Streptomyces coelicolor A3(2) SC5A7.19c	32.6	55.7	212	transcriptional regulator
2902	6402	2808364	2807426	939	sp:PT56_YEAST	Saccharomyces cerevisiae YOR201C PET56	22.8	47.3	334	ribosomal RNA ribose methylase or tRNA/rRNA methyltransferase
2903	6403	2809778	2808399	1380	sp:SYC_ECOLI	Escherichia coli K12 cysS	42.2	68.8	464	cysteinyl-tRNA synthetase
2904	6404	2811806	2809824	1983	prf:2511335C	Lactococcus lactis sacB	47.0	77.0	668	PTS system, enzyme II sucrose protein (sucrose-specific IIABC component)
2905	6405	2813258	2811960	1299	gp:AF205034_4	Clostridium acetobutylicum ATCC 824 scrB	35.3	56.9	473	sucrose 6-phosphate hydrolase or sucrase
2906	6406	2814037	2813279	759	sp:NAGB_ECOLI	Escherichia coli K12 nagB	38.3	69.4	248	glucosamine-6-phosphate isomerase
2907	6407	2815232	2814081	1152	sp:NAGA_VIBFU	Vibrio furnissii SR1514 manD	30.2	60.3	368	N-acetylglucosamine-6-phosphate deacetylase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2908	6408	2815458	2816393	936	sp DAPA_ECOLI	Escherichia coli K12 dapA	28.2	62.1	298	dihydrodipicolinate synthase
2909	6409	2816409	2817317	909	sp GLK_STRCO	Streptomyces coelicolor A3(2) SC6E10 20c glk	28.7	57.6	321	glucokinase
2910	6410	2817363	2818058	696	prf 2516292A	Clostridium perfringens NCTC 8798 nanE	36.4	68.6	220	N-acetylmannosamine-6 phosphate epimerase
2911	6411	2818313	2818137	177						
2912	6412	2819564	2818350	1215	sp NANH_MICVI	Micromonospora viridifaciens ATCC 31146 nadA	24.8	50.3	439	sialidase precursor
2913	6413	2820285	2819557	729	gp AF181498_1	Rhizobium etli ansR	26.6	57.2	222	L-asparagine permease operon repressor
2914	6414	2820584	2822191	1608	gp BFU64514_1	Bacillus firmus OF4 dppA	22.5	51.4	560	dipeptide transporter protein or heme-binding protein
2915	6415	2822387	2823337	951	sp OPPB_BACFI	Bacillus firmus OF4 dappB	31.9	64.3	342	dipeptide transport system permease protein
2916	6416	2824274	2825341	1068	sp OPPD_BACSU	Bacillus subtilis 168 oppD	46.5	78.3	314	oligopeptide transport ATP-binding protein
2917	6417	2825341	2826156	816	sp OPPF_LACLA	Lactococcus lactis oppF	43.4	78.7	258	oligopeptide transport ATP-binding protein
2918	6418	2826835	2826215	621	sp RHTB_ECOLI	Escherichia coli K12 rhtB	28.5	62.7	193	homoserine/homoserin lactone efflux protein or lysE type translocator
2919	6419	2826922	2827404	483	prf 2309333A	Bradyrhizobium japonicum lrp	31.0	66.2	142	leucine-responsive regulatory protein
2920	6420	2827817	2827458	360						
2921	6421	2828383	2827904	480	pir C70607	Mycobacterium tuberculosis H37Rv Rv3581c	55.9	86.2	152	hypothetical protein
2922	6422	2829146	2828379	768	sp Y18T_MYCTU	Mycobacterium tuberculosis H37Rv Rv3582c	46.4	71.5	235	hypothetical protein
2923	6423	2829749	2829156	594	pir H70803	Mycobacterium tuberculosis H37Rv Rv3583c	73.3	91.1	157	transcription factor

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Termina (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
2924	6424	2830057	2830779	723	pir|S14394|A	Mycobacterium tuberculosis H37Rv Rv3246c mtrA	43.5	70.0	223	two-component system response regulator
2925	6425	2830779	2831894	1116	sp|BAES_ECOLI	Escherichia coli K12 baeS	29.3	67.7	341	two-component system sensor histidine kinase
2926	6426	2832085	2832666	582						
2927	6427	2832790	2834181	1392	sp|RADA_ECOLI	Escherichia coli K12 radA	41.5	74.3	463	DNA repair protein RadA
2928	6428	2834188	2835225	1038	sp|YACK_BACSU	Bacillus subtilis 168 yacK	40.3	73.3	345	hypothetical protein
2929	6429	2835969	2835283	687	pir|D70804	Mycobacterium tuberculosis H37Rv Rv3587c	29.4	53.3	231	hypothetical protein
2930	6430	2837499	2836048	1452	gp|PPU96338_1	Pseudomonas putida NCIMB 9866 plasmid pRA4000	59.5	85.1	471	p-hydroxybenzaldehyde dehydrogenase
2931	6431	2837737	2837591	147						
2932	6432	2838576	2837956	621	pir|T08204	Chlamydomonas reinhardtii ca1	36.7	66.2	210	mitochondrial carbonate dehydratase beta
2933	6433	2838643	2839521	879	gp|AF121797_1	Streptomyces antibioticus IMRU 3720 mutY	48.4	70.7	283	A/G-specific adenine glycosylase
2934	6434	2839562	2840716	1155						
2935	6435	2841063	2840758	306						
2936	6436	2841075	2841848	774	gp|AB009078_1	Brevibacterium saccharolyticum	99.2	99.6	258	L-2,3-butanediol dehydrogenase
2937	6437	2842130	2842453	324						
2938	6438	2842493	2843233	741						
2939	6439	2843405	2843716	312						
2940	6440	2843722	2843432	291	pir|E70552	Mycobacterium tuberculosis H37Rv Rv3592	48.5	69.1	97	hypothetical protein
2941	6441	2845139	2845558	420	GSP|Y29188	Pseudomonas aeruginosa ORF24222	57.0	63.0	99	virulence factor
2942	6442	2845889	2846101	213	GSP|Y29193	Pseudomonas aeruginosa ORF25110	54.0	55.0	72	virulence factor

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2943	6443	2846180	2846506	327	GSP:Y29193	Pseudomonas aeruginosa ORF25110	74 0	75 0	55	virulence factor
2944	6444	2845940	2844166	2775	sp MECB_BACSU	Bacillus subtilis 168 mecB	58 5	86 2	832	ClpC adenosine triphosphatase / ATP-binding proteinase
2945	6445	2847229	2848659	1431	gp AB035643_1	Bacillus cereus ts-4 impdh	37 1	70 2	469	inosine monophosphate dehydrogenase
2946	6446	2848759	2849779	1011	pir C6117	Rhodococcus rhodochrous nitR	24 7	62 7	316	transcription factor
2947	6447	2850031	2851815	1785	sp PH2M_TRICU	Trichosporon cutaneum ATCC 46490	33 5	60 9	680	phenol 2-monooxygenase
2948	6448	2852017	2853732	1716						
2949	6449	2853769	2855709	1941						
2950	6450	2855795	2857516	1722						
2951	6451	2859044	2859205	162						
2952	6452	2859055	2857613	1443	gp AF237667_1	Corynebacterium glutamicum lmrB	100 0	100 0	481	lincomycin resistance protein
2953	6453	2860145	2859195	951	pir G70807	Mycobacterium tuberculosis H37Rv Rv3517	26 7	55 8	240	hypothetical protein
2954	6454	2862082	2860505	1578	gp AB012100_1	Bacillus stearothermophilus lysS	41 7	71 2	511	lysyl-tRNA synthetase
2955	6455	2862929	2862132	798	gp CGPAN_2	Corynebacterium glutamicum ATCC 13032 panC	29 9	52 6	268	pantoate--beta-alanine ligase
2956	6456	2863621	2862929	693						
2957	6457	2864421	2863624	798						
2958	6458	2864848	2864384	465	gp MLCB2548_4	Mycobacterium leprae MLCB2548 04c	29 0	69 6	138	hypothetical membrane protein
2959	6459	2865343	2864867	477	sp HPPK_METEX	Methylobacterium extorquens AM1 folK	42 4	69 0	158	2-amino-4 hydroxy 6 hydroxymethyldihydropteridine pyrophosphokinase
2960	6460	2865735	2865346	390	sp FOLB_BACSU	Bacillus subtilis 168 folB	38 1	69 5	118	dihydroneopterin aldolase
2961	6461	2866567	2865731	837	gp AB028656_1	Mycobacterium leprae folP	51 5	75 0	268	dihydropteroate synthase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
2962	6462	2867173	2866586	588	sp GCH1_BACSU	Bacillus subtilis 168 mtrA	60.6	86.2	188	GTP cyclohydrolase I
2963	6463	2867471	2868385	915						
2964	6464	2869748	2867169	2580			56.0	69.0	782	cell division protein FtsH
2965	6465	2870444	2869863	582	gp AF008931_1	Salmonella typhimurium GP660 hprt	51.5	83.0	165	hypoxanthine phosphoribosyltransferase
2966	6466	2871389	2870499	891	sp YZC5_MYCTU	Mycobacterium tuberculosis H37Rv Rv3625c	41.0	66.8	310	cell cycle protein MesJ or cytosine deaminase-related protein
2967	6467	2872677	2871445	1233	sp DAC_ACTSP	Actinomadura sp. R39 dac	27.2	51.4	459	D alanyl-D-alanine carboxypeptidase
2968	6468	2873376	2873399	474	sp PYR_ECOLI	Escherichia coli K12 ppa	49.7	73.6	159	inorganic pyrophosphatase
2969	6469	2873611	2873393	219						
2970	6470	2875443	2873905	1539	pir H70886	Mycobacterium tuberculosis H37Rv speE	56.0	80.7	507	spermidine synthase
2971	6471	2875932	2875434	399	sp YOB1_MYCTU	Mycobacterium tuberculosis H37Rv Rv2600	38.6	86.4	132	hypothetical membrane protein
2972	6472	2876280	2875870	411	sp YOB2_MYCTU	Mycobacterium tuberculosis H37Rv Rv2599	36.8	63.2	144	hypothetical protein
2973	6473	2876777	2876280	498	sp YOB3_MYCTU	Mycobacterium tuberculosis H37Rv Rv2598	36.4	60.1	173	hypothetical protein
2974	6474	2877385	2876777	609	sp YOB4_MYCTU	Mycobacterium tuberculosis H37Rv Rv2597	44.6	72.3	202	hypothetical protein
2975	6475	2877703	2877455	249	sp PTBA_BACSU	Bacillus subtilis 168 bglP	30.3	59.6	89	PTS system, beta glucosides-permease II ABC component
2976	6476	2877858	2877595	264						
2977	6477	2879710	2878478	1233	gp AB017795_2	Nocardioides sp. KP7 phdD	38.0	69.6	411	ferredoxin reductase
2978	6478	2879965	2880252	288	gp SCH69_9	Streptomyces coelicolor A3(2) SCH69.09c	46.4	73.2	97	hypothetical protein
2979	6479	2880544	2880987	444	prf 2516298U	Burkholderia pseudomallei ORF E	26.7	59.3	135	bacterial regulatory protein, marR family

Table 1 (continued)

SEQ NO (DNA)	SEQ NC (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
2980	6480	2880998	2884882	3885	prf 2413335A	Streptomyces roseosporus cpsB	28 4	51 6	1241	peptide synthase
2981	6481	2883304	2881844	1461						
2982	6482	2886497	2884935	1563	prf 2310295A	Escherichia coli K12 padA	35 0	63 7	488	phenylacetaldehyde dehydrogenase
2983	6483	2887833	2886916	918	gp CJ11168X2_25 4	Campylobacter jejuni Cj0604	57 3	79 7	241	hypothetical protein
2984	6484	2890185	2890346	162	GP MSGTCWPA_1	Mycobacterium tuberculosis	62 0	63 0	54	hypothetical protein
2985	6485	2890377	2890553	177	GP MSGTCWPA_1	Mycobacterium tuberculosis	74 0	80 0	31	hypothetical protein
2986	6486	2890540	2888897	1644	gsp R94368	Brevibacterium flavum MJ-233	99 5	100 0	548	heat shock protein or chaperon or groEL protein
2987	6487	2890930	2890751	180						
2988	6488	2892138	2890930	1209						
2989	6489	2893100	2892138	963						
2990	6490	2895085	2893100	1986						
2991	6491	2897525	2895072	2454						
2992	6492	2900326	2897528	2799						
2993	6493	2903920	2900330	3591	prf 2309326A	Homo sapiens MUC5B	21 7	42 3	1235	hypothetical protein
2994	6494	2906738	2903964	2775						
2995	6495	2907250	2906639	612						
2996	6496	2907515	2908885	1371	pir G70870	Mycobacterium tuberculosis H37Rv Rv2522c	37 1	68 0	447	peptidase
2997	6497	2909210	2909788	579						
2998	6498	2909830	2909231	600						
2999	6499	2910172	2913228	3057	prf 2504285E	Staphylococcus aureus mnhA	35 6	68 3	797	Na+/H+ antiporter or multiple resistance and pH regulation related protein A or NADH dehydrogenase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
3000	6500	2913235	2913723	489	gp AF097740_3	Bacillus firmus OF4 mrpC	44.2	81.7	104	Na+/H+ antiporter or multiple resistance and pH regulation related protein C or cation transport system protein
3001	6501	2913749	2915416	1668	gp AF097740_4	Bacillus firmus OF4 mrpD	35.2	72.1	523	Na+/H+ antiporter or multiple resistance and pH regulation related protein D
3002	6502	2915482	2915922	441	gp AF097740_5	Bacillus firmus OF4 mrpE	26.7	60.9	161	Na+/H+ antiporter or multiple resistance and pH regulation related protein E
3003	6503	2915929	2916201	273	prf 2416476G	Rhizobium meliloti phaF	32.5	66.2	77	K+ efflux system or multiple resistance and pH regulation related protein F
3004	6504	2916205	2916582	378	prf 2504285H	Staphylococcus aureus mnhG	25.6	63.6	121	Na+/H+ antiporter or multiple resistance and pH regulation related protein G
3005	6505	2917617	2917024	594	pir D70594	Mycobacterium tuberculosis H37Rv lipV	24.7	54.5	178	hypothetical protein
3006	6506	2918757	2917630	1128	sp YBDK_ECOLI	Escherichia coli K12 ybdK	27.0	61.7	334	hypothetical protein
3007	6507	2919481	2918819	663						
3008	6508	2919715	2920293	579	sp DEF_BACSU	Bacillus subtilis 168 def	37.5	60.9	184	polypeptide deformylase
3009	6509	2919741	2919490	252	pir D70631	Mycobacterium tuberculosis H37Rv Rv0430	47.9	70.4	71	hypothetical protein
3010	6510	2920286	2921290	1005	pir B70631	Mycobacterium tuberculosis H37Rv Rv0428c	31.3	54.2	339	acetyltransferase (GNAT) family or N terminal acetylating enzyme
3011	6511	2920476	2919808	669						
3012	6512	2920849	2920220	630						
3013	6513	2921320	2922108	789	gp AF108767_1	Salmonella typhimurium LT2 xthA	30.8	59.9	31	exodeoxyribonuclease III or exonuclease
3014	6514	2922118	2923617	1500	gp BEU88888_2	Bacillus firmus OF4 cls	27.9	62.0	513	cardiolipin synthase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
3015	6515	2924191	2924844	654						
3016	6516	2925147	2923954	1194	sp BCR_ECOLI	Escherichia coli K12 bcr	31.6	67.2	393	membrane transport protein or bicyclomycin resistance protein
3017	6517	2925541	2926704	1164	gp VCAJ10968_1	Vibrio cholerae JS1569 nptA	28.5	68.9	382	sodium dependent phosphate pump
3018	6518	2927546	2926707	840	sp PHZC_PSEAR	Pseudomonas aureofaciens 30-84 phzC	38.8	56.4	289	phenazine biosynthesis protein
3019	6519	2928283	2927651	633						
3020	6520	2928318	2927551	768	gp SCE8_16	Streptomyces coelicolor A3(2) SCE8.16c	24.3	60.8	255	ABC transporter
3021	6521	2929237	2928302	936	sp BCRA_BACLI	Bacillus licheniformis ATCC 9945A bcrA	36.9	66.3	309	ABC transporter ATP binding protein
3022	6522	2929756	2929256	501	pir C70629	Mycobacterium tuberculosis H37Rv Rv0413	47.6	68.5	168	mutator mutT protein
3023	6523	2929951	2931336	1386	pir B70629	Mycobacterium tuberculosis H37Rv Rv0412c	35.0	70.2	423	hypothetical membrane protein
3024	6524	2931340	2932371	1032	sp GLNH_BACST	Bacillus stearothermophilus NUB36 glnH	31.5	64.8	270	glutamine-binding protein precursor
3025	6525	2932577	2934829	2253	pir H70628	Mycobacterium tuberculosis H37Rv Rv0410c pknG	41.2	63.5	805	serine/threonine kinase
3026	6526	2933398	2932652	747						
3027	6527	2938403	2939767	1365	sp ADRO_BOVIN	Bos taurus	37.2	67.8	457	ferredoxin/ferredoxin-NADP reductase
3028	6528	2939907	2940452	546	sp ELAA_ECOLI	Escherichia coli K12 elaA	34.0	60.3	156	acetyltransferase (GNAT) family
3029	6529	2941508	2940447	1062						
3030	6530	2942500	2941472	1029						
3031	6531	2943007	2942609	399						
3032	6532	2944205	2943012	1194	sp PURT_BACSU	Bacillus subtilis 168 purT	59.1	82.6	379	phosphoribosylglycinamide formyltransferase
3033	6533	2946526	2945639	888						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
3034	6534	2947591	2946698	894	pir S60890	Corynebacterium glutamicum orf2	77.6	90.9	295	insertion element (IS3 related)
3035	6535	2947886	2947620	267	pir S60889	Corynebacterium glutamicum orf1	67.4	84.3	89	insertion element (IS3 related)
3036	6536	2949188	2948049	1140	gp AB015841_1	Streptomyces thermoviolaceus opc-520 chiS	22.4	51.3	349	two-component system sensor histidine kinase
3037	6537	2949882	2949265	618	sp DEGU_BACBR	Bacillus brevis ALK36 degU	31.7	65.6	218	transcriptional regulator
3038	6538	2950297	2950431	225						
3039	6539	2951723	2950434	1290	gp AB003160_1	Corynebacterium ammoniagenes purA	89.7	95.3	427	adenylosuccinate synthetase
3040	6540	2951933	2952691	759	pir G70575	Mycobacterium tuberculosis H37Rv Rv0358	34.3	59.3	204	hypothetical protein
3041	6541	2952709	2952972	264						
3042	6542	2954141	2952975	1167	sp YEDA_CORGL	Corynebacterium glutamicum AS019 ATCC 13059 ORF3	100.0	100.0	359	hypothetical membrane protein
3043	6543	2955272	2954241	1032	pir S09283	Corynebacterium glutamicum AS019 ATCC 13059 fda	99.7	100.0	344	fructose-bisphosphate aldolase
3044	6544	2956473	2955523	951	gp CGFDA_1	Corynebacterium glutamicum AS019 ATCC 13059 ORF1	100.0	100.0	304	hypothetical protein
3045	6545	2957447	2956830	618	pir G70833	Mycobacterium tuberculosis H37Rv Rv0380c	76.9	91.2	182	methyltransferase
3046	6546	2958036	2957485	552	gp AF058713_1	Pyrococcus abyssi pyrE	39.1	65.5	174	orotate phosphoribosyltransferase
3047	6547	2959110	2958139	972	pir B70834	Mycobacterium tuberculosis H37Rv Rv0383c	27.6	60.0	250	hypothetical protein
3048	6548	2960371	2959520	852	sp THTM_HUMAN	Homo sapiens mpsT	29.6	56.1	294	3-mercaptopyruvate sulfurtransferase
3049	6549	2961187	2960468	720						
3050	6550	2963009	2962730	279						
3051	6551	2963596	2963198	399						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
3052	6552	2964258	2964434	177	GSP:Y29188	Pseudomonas aeruginosa ORF24222	76.0	82.0	59	virulence factor
3053	6553	2965076	2965837	762	GSP:Y29182	Pseudomonas aeruginosa ORF23228	38.0	55.0	200	virulence factor
3054	6554	2965188	2965583	396	GSP:Y29193	Pseudomonas aeruginosa ORF25110	62.0	63.0	132	virulence factor
3055	6555	2967804	2966458	1347	pir S76683	Synechocystis sp. PCC6803 slr0525	24.7	54.8	489	sodium/glutamate symport carrier protein
3056	6556	2968403	2968789	387	sp CADF_STAAU	Staphylococcus aureus cadC	37.0	71.3	108	cadmium resistance protein
3057	6557	2968951	2969808	858	pir H75109	Pyrococcus abyssi Orsay PAB0462	23.7	63.3	283	cation efflux system protein (zinc/cadmium)
3058	6558	2969834	2971003	1170	gp AB010439_1	Rhodococcus rhodochrous IFO3338	22.5	45.4	476	monooxygenase or oxidoreductase or steroid monooxygenase
3059	6559	2971017	2972057	1041	sp LUXA_KRYAS	Kryptophanaron alfredi symbiont luxA	21.1	47.4	399	alkanal monooxygenase alpha chain
3060	6560	2972099	2971338	762						
3061	6561	2973209	2972060	1146	sp METB_ECOLI	Escherichia coli K12 metB	36.5	62.4	375	cystathionine gamma-lyase
3062	6562	2973706	2973230	567	gp SC1A2_11	Streptomyces coelicolor A3(2) SC1A2.11	40.2	67.9	184	bacterial regulatory protein, lacI family
3063	6563	2973961	2974200	240	gp SCE20_34	Streptomyces coelicolor A3(2) SCE20.34c arr	49.4	65.2	89	rifampin ADP-ribosyl transferase
3064	6564	2974200	2974382	183	gp SCE20_34	Streptomyces coelicolor A3(2) SCE20.34c arr	73.2	87.5	56	rifampin ADP-ribosyl transferase
3065	6565	2974467	2975591	1125	pir E70812	Mycobacterium tuberculosis H37Rv Rv0837c	30.5	56.2	361	hypothetical protein
3066	6566	2975629	2976360	732	pir D70812	Mycobacterium tuberculosis H37Rv Rv0836c	33.8	64.7	204	hypothetical protein
3067	6567	2976596	2977774	1179	pir D70834	Mycobacterium tuberculosis H37Rv Rv0385	31.9	60.6	386	oxidoreductase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
3068	6568	2978644	2977847	798	pir B69109	Methanobacterium thermoautotrophicum Delta H MTH1811	32.0	67.3	275	N-carbamoyl-D-amino acid amidohydrolase
3069	6569	2978737	2978979	243						
3070	6570	2979982	2980115	1134	gp SC4A7_3	Streptomyces coelicolor A3(2) SC4A7.03	28.0	55.4	289	hypothetical protein
3071	6571	2980387	2981216	330	GP ABCARRA_2	Azospirillum brasilense carR	38.0	44.0	108	novel two-component regulatory system
3072	6572	2981698	2980181	1518	prf 2104333D	Rhodococcus erythropolis thcA	69.6	90.3	507	aldehyde dehydrogenase
3073	6573	2982460	2982023	438	gp SAU43299_2	Streptomyces albus G hspR	47.4	70.4	135	heat shock transcription regulator
3074	6574	2983679	2982495	1185	sp DNAJ_MYCTU	Mycobacterium tuberculosis H37Rv RV0352 dnaJ	56.7	80.1	397	heat shock protein dnaJ
3075	6575	2984522	2983887	636	sp GRPE_STRCO	Streptomyces coelicolor grpE	38.7	66.5	212	nucleotide exchange factor grpE protein bound to the ATPase domain of the molecular chaperone DnaK
3076	6576	2986397	2984544	1854	gsp R94587	Brevibacterium flavum MJ-233 dnaK	99.8	99.8	618	heat shock protein dnaK
3077	6577	2986833	2988164	1332	gp SCF6_8	Streptomyces coelicolor A3(2) SCF6.09	42.6	79.0	338	hypothetical membrane protein
3078	6578	2988846	2988214	633	sp PFS_HELPY	Helicobacter pylori HP0089 mtn	27.2	60.0	195	5'-methylthioadenosine nucleosidase and S-adenosylhomocysteine nucleosidase
3079	6579	2990045	2988846	1200						
3080	6580	2991718	2992602	885						
3081	6581	2993286	2989954	3333	sp CUT3_SCHPO	Schizosaccharomyces pombe cut3	18.9	48.4	1311	chromosome segregation protein
3082	6582	2993921	2993286	636						
3083	6583	2995405	2993921	1485						
3084	6584	2996781	2995747	1035	sp ADH2_BACST	Bacillus stearothermophilus DSM 2334 adh	50.0	81.7	334	alcohol dehydrogenase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
3085	6585	2997151	2997366	216						
3086	6586	2997687	2997481	207						
3087	6587	2997688	2997876	189						
3088	6588	2998223	2997963	261						
3089	6589	2999454	2998528	927	pir|B69997	Bacillus subtilis ytnM	43.5	70.1	301	hypothetical membrane protein
3090	6590	3000200	2999478	723	gp|SC7A8_10	Streptomyces coelicolor A3(2) SC7A8.10c	32.5	53.2	252	hypothetical protein
3091	6591	3001512	3002426	915						
3092	6592	3001539	3000241	1299	sp|CYSN_ECOLI	Escherichia coli K12 cysN	47.3	78.3	414	sulfate adenylyltransferase, subunit 1
3093	6593	3002453	3001542	912	sp|CYSD_ECOLI	Escherichia coli K12 cysD	46.1	70.1	308	sulfate adenylyltransferase small chain
3094	6594	3003145	3002453	693	sp|CYH1_BACSU	Bacillus subtilis cysH	39.2	64.2	212	phosphoadenosine phosphosulfate reductase
3095	6595	3005162	3003480	1683	sp|NIR_SYNP7	Synechococcus sp. PCC 7942	34.5	65.5	502	ferredoxin--nitrate reductase
3096	6596	3005545	3006915	1371	sp|ADRO_YEAST	Saccharomyces cerevisiae FL200 arh1	30.8	61.4	487	ferredoxin/ferredoxin-NADP reductase
3097	6597	3007294	3008376	1083	prf|2420294J	Homo sapiens hypE	32.6	59.7	144	huntingtin interactor
3098	6598	3008689	3008453	237						
3099	6599	3008770	3009303	534						
3100	6600	3009162	3008749	414	sp|PHNB_ECOLI	Escherichia coli K12 phnB	26.8	59.9	142	alkylphosphonate uptake protein and C-P lyase activity
3101	6601	3009242	3009607	366	gp|SCE68_10	Streptomyces coelicolor A3(2) SCE68.10	50.0	66.3	80	hypothetical protein
3102	6602	3010231	3009710	522	gp|PPAMOA_1	Pseudomonas putida DSMZ ID 88-260 amoA	39.1	76.4	161	ammonia monooxygenase
3103	6603	3010659	3010979	321						
3104	6604	3010926	3010441	486						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
3105	6605	3010989	3011273	285	SP YTZ3_AGRVI	Agrobacterium vitis ORFZ3	41.0	58.0	68	hypothetical protein
3106	6606	3011805	3011242	564						
3107	6607	3012809	3011808	1002	sp YGB7_ALCEU	Alcaligenes eutrophus H16 ORF7	26.1	57.9	337	hypothetical protein
3108	6608	3013798	3013106	693	gp HIU68399_3	Haemophilus influenzae hmcB	35.7	64.8	199	ABC transporter
3109	6609	3014550	3013837	714	gp HIU68399_3	Haemophilus influenzae hmcB	39.3	73.0	211	ABC transporter
3110	6610	3014616	3015824	1209	pir A69778	Bacillus subtilis ydeG	30.8	67.8	416	metabolite transport protein homolog
3111	6611	3015469	3014648	822						
3112	6612	3016238	3016924	687						
3113	6613	3017149	3015827	1323	sp DAPF_ECOL	Escherichia coli K12 msgB	21.5	48.5	466	succinyl-diaminopimelate desuccinylase
3114	6614	3017316	3019220	1905						
3115	6615	3017539	3018312	774						
3116	6616	3018181	3017420	762						
3117	6617	3019076	3018123	954	GPU DCA297422_ 1	Daucus carota	33.0	46.0	114	dehydrin-like protein
3118	6618	3020609	3019542	1068	sp MALK_ECOLI	Escherichia coli K12 malK	24.9	50.1	373	maltose/maltodextrin transport ATP-binding protein
3119	6619	3021202	3020561	642						
3120	6620	3021825	3021208	618	gp AF036485_6	Lactococcus lactis Plasmid pNZ4000 Orf-200 cbiM	30.2	67.6	179	cobalt transport protein
3121	6621	3022929	3022113	816	sp FRP_VIBHA	Vibrio harveyi MAV frp	37.2	71.4	231	NADPH-flavin oxidoreductase
3122	6622	3023900	3022998	903	sp IUNH_CRIFA	Crithidia fasciculata iunH	28.4	59.3	317	inosine-uridine preferring nucleoside hydrolase
3123	6623	3024379	3025353	975	gp SCE20_8	Streptomyces coelicolor A3(2) SCE20.08c	31.2	59.4	276	hypothetical membrane protein
3124	6624	3025552	3026130	588	sp 3MG1_ECOLI	Escherichia coli K12 tag	50.3	78.8	179	DNA-3-methyladenine glycosylase
3125	6625	3027299	3026142	1158	sp HMPA_ALCEU	Alcaligenes eutrophus H16 fhp	33.5	63.8	406	flavohemoprotein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (aa)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (aa)	Function
3125	6626	3027561	3028163	603						
3127	6627	3028228	3028851	624	gp SCO276673_18 mmyQ	Streptomyces coelicolor A3(2) mmyQ	34 8	63 8	210	oxidoreductase
3129	6628	3028878	3029033	156						
3129	6629	3029474	3028884	591	sp BGLG_ECOLI	Escherichia coli K12 bglC	28 1	69 3	192	transcription antiterminator or beta-glucoside positive regulatory protein
3130	6630	3029504	3029782	279						
3131	6631	3030061	3029702	360	sp ABGA_CLOLO abgA	Clostridium longisporum B6405 abgA	43 7	59 9	167	6-phospho beta glucosidase
3132	6632	3030155	3030535	381						
3133	6633	3030340	3030101	240	sp ABGA_CLOLO abgA	Clostridium longisporum B6405 abgA	43 9	78 8	66	6-phospho beta-glucosidase
3134	6634	3030723	3031979	1257	gp L78665_2	Methylobacillus flagellatus aat	53 7	80 9	402	aspartate aminotransferase
3135	6635	3032647	3032348	300						
3136	6636	3032664	3033863	1203	gp AF189147_1	Corynebacterium glutamicum ATCC 13032 tnp	100 0	100 0	401	transposase (ISCg2)
3137	6637	3034181	3035437	1257	gp SCQ11_10	Streptomyces coelicolor A3(2) SCQ11 10c	33 6	70 2	399	hypothetical membrane protein
3138	6638	3034287	3034105	183						
3139	6639	3036756	3035440	1317	prf 2422381B	Sinorhizobium meliloti rkpK	40 5	72 2	442	UDP-glucose dehydrogenase
3140	6640	3037411	3036645	567	sp DCD_ECOLI	Escherichia coli K12 dcd	43 6	72 3	188	deoxycytidine triphosphate deaminase
3141	6641	3037675	3037911	237						
3142	6642	3038172	3038942	771	gp SCC75A_16	Streptomyces coelicolor A3(2) SCC75A 16c	30 6	59 4	229	hypothetical protein
3143	6643	3040681	3038993	1689						
3144	6644	3041932	3040748	1185	gp AB008771_1	Streptomyces thermoviolaceus nagA	28 5	58 1	410	beta-N-Acetylglucosaminidase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
3145	6645	3041994	3042437	444						
3146	6646	3042503	3042703	201						
3147	6647	3042690	3045788	3129	gp MLCB1883_7	Mycobacterium leprae MLCB1883.13c	29.6	49.4	1416	hypothetical protein
3148	6648	3043642	3043022	621						
3149	6649	3045796	3045990	195						
3150	6650	3047146	3048648	903	gp MLCB1883_4	Mycobacterium leprae MLCB1883.05c	24.8	47.1	363	hypothetical membrane protein
3151	6651	3047189	3046122	1068	pir JC4001	Streptomyces sp. acyA	27.7	51.0	408	acyltransferase or macrolide 3-O-acyltransferase
3152	6652	3047904	3047197	708						
3153	6653	3048058	3049479	1422	gp MLCB1883_3	Mycobacterium leprae MLCB1883.04c	31.2	54.8	529	hypothetical membrane protein
3154	6654	3050522	3051190	669						
3155	6655	3050592	3049456	1137	pir G70961	Mycobacterium tuberculosis H37Rv Rv0225	53.4	79.1	369	hexosyltransferase
3156	6656	3051194	3051964	771	pir F70961	Mycobacterium tuberculosis H37Rv Rv0224c	58.6	73.3	251	methyl transferase
3157	6657	3053891	3052062	1830	sp PPCK_NEOFR	Neocallimastix frontalis pepck	54.7	78.5	601	phosphoenolpyruvate carboxykinase (GTP)
3158	6658	3054759	3055769	1011	pir E75125	Pyrococcus abyssi Orsay PAB2393	24.4	52.7	332	C4-dicarboxylate transporter
3159	6659	3055867	3056631	765	sp YGGH_ECOLI	Escherichia coli K12 yggH	35.7	67.2	241	hypothetical protein
3160	6660	3056613	3057317	705	pir E70959	Mycobacterium tuberculosis H37Rv Rv0207c	69.1	85.0	207	hypothetical protein
3161	6661	3057328	3059643	2316	pir C70839	Mycobacterium tuberculosis H37Rv Rv0206c mmpL3	42.3	72.3	768	mebrane transport protein
3162	6662	3059517	3058096	1422						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
3163	6663	3059651	3060733	1083	pir A70839	Mycobacterium tuberculosis H37Rv Rv0204c	29 1	62 9	364	hypothetical membrane protein
3164	6664	3060733	3061095	363	pir H70633	Mycobacterium tuberculosis H37Rv Rv0401	34 3	69 4	108	hypothetical membrane protein
3165	6665	3062927	3061380	1548	gp AF113605_1	Streptomyces coelicolor A3(2) pccB	49 7	76 9	523	propionyl CoA carboxylase complex B subunit
3166	6666	3067780	3062951	4830	sp ERY1_SACER	Streptomyces erythraeus eryA	30 2	54 2	1747	polyketide synthase
3167	6667	3069930	3068143	1788	pir S10345A	Mycobacterium bovis BCG	33 5	62 3	592	acyl-CoA synthase
3168	6668	3071140	3070214	927	pir F70887	Mycobacterium tuberculosis H37Rv Rv3802c	39 8	67 4	319	hypothetical protein
3169	6669	3071644	3071147	498						
3170	6670	3073620	3071650	1971	sp CSP1_CORGL	Corynebacterium glutamicum (Brevibacterium flavum) ATCC 17965 cop1	98 6	99 5	657	major secreted protein PS1 protein precursor
3171	6671	3074047	3075447	1401						
3172	6672	3074675	3073857	819						
3173	6673	3076562	3075540	1023	sp A85C_MYCTU	Mycobacterium tuberculosis ERDMANN RV0129C fbpC	36 3	62 5	331	antigen 85-C
3174	6674	3078772	3076715	2058	pir A70888	Mycobacterium tuberculosis H37Rv Rv3805c	37 5	61 2	667	hypothetical membrane protein
3175	6675	3079848	3078853	996	sp NOEC_AZOCA	Azorhizobium caulinodans ORS571 noeC	27 1	51 5	295	nodulation protein
3176	6676	3080351	3079848	504	pir C70888	Mycobacterium tuberculosis H37Rv Rv3807c	51 2	75 0	168	hypothetical protein
3177	6677	3082311	3080344	1968	pir D70888	Mycobacterium tuberculosis H37Rv Rv3808c	55 6	74 7	656	hypothetical protein
3178	6678	3082467	3083960	1494						
3179	6679	3084411	3083935	477	sp BCRC_BACLI	Bacillus licheniformis ATCC 9945A bcrC	28 2	56 5	170	phosphatidic acid phosphatase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
3180	6680	3085200	3084424	777						
3181	6681	3085727	3085218	510						
3182	6682	3086747	3087048	1302	sp FMO1_PIG	Sus scrofa fmo1	24.4	50.4	377	dimethylaniline monooxygenase (N-oxide-forming)
3183	6683	3087665	3088276	612						
3184	6684	3088303	3087101	1203	sp GLF_ECOLI	Escherichia coli K12 glf	43.2	72.9	377	UDP-galactopyranose mutase
3185	6685	3088616	3090664	2049	pir G70520	Mycobacterium tuberculosis H37Rv Rv3811 csp	29.6	47.8	659	hypothetical protein
3186	6686	3092286	3090760	1527	sp GLPK_PSEAE	Pseudomonas aeruginosa ATCC 15692 glpK	51.7	78.8	499	glycerol kinase
3187	6687	3093175	3092342	834	pir A70521	Mycobacterium tuberculosis H37Rv Rv3813c	41.6	70.3	279	hypothetical protein
3188	6688	3094050	3093175	876	pir D70521	Mycobacterium tuberculosis H37Rv Rv3816c	46.7	72.0	261	acyltransferase
3189	6689	3095343	3094078	1266	gsp W26465	Mycobacterium tuberculosis H37Rv	70.2	87.6	419	seryl-tRNA synthetase
3190	6690	3095574	3096287	714	sp FARR_ECOLI	Escherichia coli K12 farR	27.7	61.7	235	transcriptional regulator, GntR family or fatty acyl-responsive regulator
3191	6691	3096311	3097423	1113	pir H70652	Mycobacterium tuberculosis H37Rv Rv3835	32.6	61.2	356	hypothetical protein
3192	6692	3097423	3097764	342	pir A70653	Mycobacterium tuberculosis H37Rv Rv3836	46.0	79.7	113	hypothetical protein
3193	6693	3097878	3097780	99						
3194	6694	3098572	3097904	669	gp AMU73808_1	Amycolatopsis methanolica pgm	37.2	62.8	218	2,3-PDG dependent phosphoglycerate mutase
3195	6695	3098825	3099454	630						
3196	6696	3099556	3100698	1143	prf 2501285A	Mycobacterium smegmatis pzaA	27.4	50.9	460	nicotinamidase or pyrazinamidase
3197	6697	3100698	3101426	729						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
3198	6698	3101734	3102768	1035	gp SC6G4_33	Streptomyces coelicolor A3(2) SC6G4 33	31.6	57.1	380	transcriptional regulator
3199	6699	3101863	3101744	120						
3200	6700	3102630	3102079	552						
3201	6701	3102894	3103763	870						
3202	6702	3103926	3104252	327	pir B26872	Streptomyces lavendulae ORF372	43.9	81.3	107	hypothetical protein
3203	6703	3104406	3105719	1314	sp AMYH_YEAST	Saccharomyces cerevisiae S288C YIR019C sta1	28.7	55.3	432	glucan 1,4-alpha-glucosidase
3204	6704	3106970	3106053	918						
3205	6705	3107769	3106951	819	sp GLPQ_BACSU	Bacillus subtilis glpQ	29.0	54.1	259	glycerophosphoryl diester phosphodiesterase
3206	6706	3108131	3109519	1389	sp GNTP_BACSU	Bacillus subtilis gntP	37.3	71.9	456	gluconate permease
3207	6707	3109464	3108823	642						
3208	6708	3109845	3110003	159						
3209	6709	3112080	3110464	1617	sp KPYK_CORGL	Corynebacterium glutamicum AS019 pyk	25.5	47.7	491	pyruvate kinase
3210	6710	3113390	3112449	942	gsp Y25997	Brevibacterium flavum lctA	99.7	99.7	314	L-lactate dehydrogenase
3211	6711	3113619	3115394	1776	pir C70893	Mycobacterium tuberculosis H37Rv Rv1069c	33.5	64.8	526	hypothetical protein
3212	6712	3115407	3116042	636	gp SC1C2_30	Streptomyces coelicolor A3(2) SC1C2 30	32.1	58.5	224	hydrolase or haloacid dehalogenase-like hydrolase
3213	6713	3116079	3116621	543	gp AF030286_1	Brevibacterium linens ORF1 tmpA	39.9	67.6	188	efflux protein
3214	6714	3116640	3117332	693	sp GLCC_ECOLI	Escherichia coli K12 MG1655 glcC	27.6	57.0	221	transcription activator or transcriptional regulator GntR family
3215	6715	3117336	3118121	786	pir B70885	Mycobacterium tuberculosis H37Rv Rv2795c	47.8	68.6	255	phosphoesterase
3216	6716	3118284	3119582	1299	sp SHIA_ECOLI	Escherichia coli K12 shiA	37.9	74.4	422	shikimate transport protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
3217	6717	3119665	3120879	1215	prf 2219306A	Neisseria meningitidis lldA	40 4	68 9	376	L-lactate dehydrogenase or FMN-dependent dehydrogenase
3218	6718	3120909	3121313	405						
3219	6719	3121538	3121909	372	sp RPC_BPPH1	Bacillus phage phi-105 ORF1	45 5	80 0	55	immunity repressor protein
3220	6720	3122129	3121992	138						
3221	6721	3123222	3123932	711						
3222	6722	3124172	3122556	1617	gp CEL Y51B11A_1	Caenorhabditis elegans Y51B11A 1	29 5	51 3	569	phosphatase or reverse transcriptase (RNA-dependent)
3223	6723	3124985	3124341	645						
3224	6724	3126298	3124897	402	sp ILL1_ARATH	Arabidopsis thaliana ill1	36 9	63 1	122	peptidase or IAA-amino acid hydrolase
3225	6725	3125343	3125492	150						
3226	6726	3126145	3125495	651	sp PMSR_ECOLI	Escherichia coli B msrA	47 6	69 1	210	peptide methionine sulfoxide reductase
3227	6727	3126392	3126991	600	pir I40858	Corynebacterium pseudodiphtheriticum sod	82 3	92 7	164	superoxide dismutase (Fe/Mn)
3228	6728	3126417	3127494	924	sp GLTC_BACSU	Bacillus subtilis gltC	32 5	65 8	292	transcriptional regulator
3229	6729	3128606	3129739	1134	gp AF121000_10	Corynebacterium glutamicum tetA	23 4	49 0	384	multidrug resistance transporter
3230	6730	3129785	3131395	1611						
3231	6731	3132920	3133030	111						
3232	6732	3133028	3131508	1521						
3233	6733	3133115	3133747	633	pir G70654	Mycobacterium tuberculosis H37Rv Rv3850	33 8	64 8	216	hypothetical protein
3234	6734	3135268	3133778	1491	prf 2508244AB	Streptomyces cyanogenus lanJ	27 3	59 3	447	membrane transport protein
3235	6735	3135297	3135752	456	sp YXAD_BACSU	Bacillus subtilis 168 yxaD	37 2	65 0	137	transcriptional regulator
3236	6736	3136491	3135856	636	prf 2518330B	Corynebacterium diphtheriae chrA	50 9	75 5	212	two-component system response regulator

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
3237	6737	3136920	3137558	639						
3238	6738	3137884	3138471	588						
3239	6739	3137903	3136593	1311	prf 2518330A	Corynebacterium diphtheriae chrS	30 2	64 5	408	two-component system sensor histidine kinase
3240	6740	3138630	3138481	150	gp SCH69_22	Streptomyces coelicolor A3(2) SCH69 22c	45 8	79 2	48	hypothetical protein
3241	6741	3139455	3138634	822	gp SCH69_20	Streptomyces coelicolor A3(2) SCH69 20c	30 0	59 2	277	hypothetical protein
3242	6742	3139951	3140952	1302	sp SP3J_BACSU	Bacillus subtilis spoIIIJ	26 0	53 6	265	stage III sporulation protein
3243	6743	3141523	3140885	639	pir C70948	Mycobacterium tuberculosis H37Rv Rv3173c	32 3	60 9	192	transcriptional repressor
3244	6744	3141969	3141709	261	sp TAG1_ECOL	Escherichia coli K12 MG1655 tag1	34 5	71 3	87	transglycosylase associated protein
3245	6745	3143356	3142454	903	sp YW12_MYCTU	Mycobacterium tuberculosis H37Rv Rv2005c	41 2	69 6	296	hypothetical protein
3246	6746	3144482	3143496	987	sp YHBW_ECOLI	Escherichia coli K12 MG1655 yhbW	38 5	73 9	314	hypothetical protein
3247	6747	3144661	3145626	966	sp YBC5_CHLVI	Chlorobium vibrioforme ybc5	28 4	51 2	334	RNA pseudouridylate synthase
3248	6748	3146569	3146841	273	GSP Y35814	Chlamydia pneumoniae	61 0	66 0	84	hypothetical protein
3249	6749	3147090	3147230	141	PIR F81737	Chlamydia muridarum Nigg TC0129	71 0	75 0	42	hypothetical protein
3250	6750	3151575	3151369	207						
3251	6751	3152204	3151842	363	sp GLCC_ECOLI	Escherichia coli K12 MG1655 glcC	30 3	56 0	109	bacterial regulatory protein, gntR family or glc operon transcriptional activator
3252	6752	3152413	3153828	1416	gp SC4G6_31	Streptomyces coelicolor SC4G6 31c	26 0	48 2	488	hypothetical protein
3253	6753	3154766	3153894	873	sp 35KD_MYCTU	Mycobacterium tuberculosis H37Rv Rv2744c	48 3	78 7	267	hypothetical protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
3254	6754	3154817	3154969	153						
3255	6755	3156697	3155246	1452						
3256	6756	3157373	3156306	1068						
3257	6757	3157471	3157223	249						
3258	6758	3157787	3157479	309						
3259	6759	3158124	3158834	711	gp SCD35_11	Streptomyces coelicolor A3(2) SCD35 11c	32.3	58.1	217	methyltransferase
3260	6760	3159800	3159081	720	sp NO21_SOYBN	soybean NO21	26.1	55.2	241	nodulin 21-related protein
3261	6761	3160219	3160419	204						
3262	6762	3160683	3161055	378						
3263	6763	3160816	3161001	186						
3264	6764	3160938	3160723	216	sp TNP5_PSEAE	Pseudomonas aeruginosa TNP5	48.2	92.9	56	transposon tn501 resolvase
3265	6765	3161219	3161701	483						
3266	6766	3161407	3161087	321	sp FER_SACER	Saccharopolyspora erythraea fer	90.3	98.4	62	ferredoxin precursor
3267	6767	3162014	3161682	333	gp SCD31_14	Streptomyces coelicolor A3(2)	47.3	85.5	55	hypothetical protein
3268	6768	3162694	3162804	111	GPU AF164956_8	Corynebacterium glutamicum Tnp1673	81.0	84.0	27	transposase
3269	6769	3162710	3162871	162	GPU AF164956_23	Corynebacterium glutamicum	84.0	90.0	46	transposase protein fragment TnpNC
3270	6770	3162852	3163889	1038						
3271	6771	3162983	3162858	126	sp G3P_PYRWO	Pyrococcus woesei gap	63.2	84.2	38	glyceraldehyde 3-phosphate dehydrogenase (pseudogene)
3272	6772	3163733	3163074	660	pir S77018	Synechocystis sp. PCC6803 sll0788	32.2	59.4	180	lipoprotein
3273	6773	3166005	3163789	2217	pir H69268	Archaeoglobus fulgidus AF0152	45.8	73.4	717	copper/potassium-transporting ATPase B or cation transporting ATPase (E1-E2 family)
3274	6774	3166437	3166267	171						

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
3275	6775	3166978	3167169	192						
3276	6776	3167646	3166450	1197	sp BAES_ECOLI	Escherichia coli K12 baeS	37.5	71.4	301	two-component system sensor histidine kinase
3277	6777	3167739	3168566	828						
3278	6778	3168401	3167646	756	sp PHOP_BACSU	Bacillus subtilis phoP	43.4	72.1	233	two-component response regulator or alkaline phosphatase synthesis transcriptional regulatory protein
3279	6779	3168669	3169340	672						
3280	6780	3169414	3170892	1479	sp COPA_PSESM	Pseudomonas syringae pv tomato copA	26.7	47.9	630	laccase or copper resistance protein precursor A
3281	6781	3171254	3171616	363	sp TLPA_BRAJA	Bradyrhizobium japonicum tlpA	31.7	63.4	101	thiol disulfide interchange protein (cytochrome c biogenesis protein)
3282	6782	3172536	3171619	918	sp QOR_MOUSE	Mus musculus qor	31.4	60.9	322	quinone oxidoreductase (NADPH quinone reductase)(zeta-crystallin)
3283	6783	3172995	3173465	471						
3284	6784	3173624	3173857	234	sp ATZN_SYNY3	Synechocystis sp PCC6803 atzN	37.2	66.7	78	zinc transporting ATPase (Zn(II)-translocating p-type ATPase
3285	6785	3174066	3174380	315						
3286	6786	3174990	3174784	207						
3287	6787	3175927	3173901	1875	sp ATZN_ECOLI	Escherichia coli K12 MG1655 atzN	39.8	68.5	606	zinc-transporting ATPase (Zn(II)-translocating p-type ATPase
3288	6788	3175643	3175254	390	PIR E72491	Aeropyrum pernix K1 APE2572	45.0	54.0	72	hypothetical protein
3289	6789	3177174	3177482	309						
3290	6790	3177304	3177089	216	GPU AF164956_8	Corynebacterium glutamicum Tnp1673	58.0	73.0	73	transposase
3291	6791	3177566	3177308	258	GPU AF164956_8	Corynebacterium glutamicum Tnp1673	75.0	77.0	70	transposase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
3292	6792	3177683	3177525	159	gp:AF121000_8	Corynebacterium glutamicum 22243 R-plasmid pAG1 tnpB	92.5	96.2	53	transposase (IS1628)
3293	6793	3178558	3178112	447	sp:THI2_ECOLI	Escherichia coli K12 thi2	39.0	74.0	100	thioredoxin
3294	6794	3178609	3178872	264						
3295	6795	3179049	3180392	1344	sp:PCAK_PSEPU	Pseudomonas putida pcaK	27.1	60.1	421	transmembrane transport protein or 4-hydroxybenzoate transporter
3296	6796	3181104	3180945	159						
3297	6797	3181126	3180551	576	sp:YQJI_ECOLI	Escherichia coli K12 yqjI	35.1	62.5	208	hypothetical protein
3298	6798	3182866	3181337	1530	sp:DNAB_ECOLI	Escherichia coli K12 dnaB	37.7	73.1	461	replicative DNA helicase
3299	6799	3183469	3183984	516						
3300	6800	3183927	3183478	450	sp:RL9_ECOLI	Escherichia coli K12 RL9	42.2	71.4	154	50S ribosomal protein L9
3301	6801	3184661	3183987	675	sp:SSB_ECOLI	Escherichia coli K12 ssb	30.6	51.5	229	single-strand DNA binding protein
3302	6802	3184985	3184701	285	sp:RS6_ECOLI	Escherichia coli K12 RS6	28.3	78.3	92	30S ribosomal protein S6
3303	6803	3185536	3185348	189						
3304	6804	3186993	3185536	1458	gp:AF187306_1	Mycobacterium smegmatis mc(2)155	41.5	68.3	480	hypothetical protein
3305	6805	3187912	3188793	882						
3306	6806	3189201	3187042	2160	sp:PBPA_BACSU	Bacillus subtilis ponA	29.1	60.1	647	penicillin-binding protein
3307	6807	3189652	3189296	357	sp:Y0HC_MYCTU	Mycobacterium tuberculosis H37Rv Rv0049	41.1	72.0	107	hypothetical protein
3308	6808	3189877	3190347	471	pir:B70912	Mycobacterium tuberculosis H37Rv Rv0042c	35.1	65.0	137	bacterial regulatory protein, marR family
3309	6809	3190378	3191319	942	sp:Y0FF_MYCTU	Mycobacterium tuberculosis H37Rv Rv2319c yofF	29.7	61.8	296	hypothetical protein
3310	6810	3191354	3191848	495						
3311	6811	3192242	3191922	321	sp:YHGC_BACSU	Bacillus subtilis yhgC	32.4	70.4	71	hypothetical protein
3312	6812	3193201	3192266	936	sp:YCEA_ECOLI	Escherichia coli K12 yceA	30.2	63.8	298	hypothetical protein
3313	6813	3194514	3193252	1263	sp:YBJZ_ECOLI	Escherichia coli K12 ybjZ	31.2	64.0	433	ABC transporter ATP-binding protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
3314	6814	3195203	3194514	690	sp YBJZ_ECOLI	Escherichia coli K12 MG1655 ybjZ	48.9	80.1	221	ABC transporter ATP-binding protein
3315	6815	3197186	3195210	1977	pir E81408	Campylobacter jejuni C;0606	18.0	42.0	237	hypothetical protein
3316	6816	3197412	3198500	1089	pir F70912	Mycobacterium tuberculosis H37Rv Rv0046c	77.8	90.0	360	hypothetical protein
3317	6817	3199187	3198582	606						
3318	6818	3200686	3199202	1485						
3319	6819	3201754	3201260	495	sp DPS_ECOLI	Escherichia coli K12 dps	37.7	64.9	154	DNA protection during starvation protein
3320	6820	3201900	3202712	813	sp FPG_ECOLI	Escherichia coli K12 mutM or fpg	28.4	55.6	268	formamidopyrimidine-DNA glycosylase
3321	6821	3202952	3204100	1149	sp RTCB_ECOLI	Escherichia coli K12 rtcB	47.5	66.6	404	hypothetical protein
3322	6822	3204067	3202979	1089						
3323	6823	3204156	3204728	573						
3324	6824	3205204	3204731	474	sp MGMT_HUMAN	Homo sapiens mgmT	38.0	63.3	166	methylated-DNA--protein-cysteine S-methyltransferase
3325	6825	3206232	3205222	1011	sp QOR_CAVPO	Cavia porcellus (Guinea pig) qor	33.3	63.6	231	zinc-binding dehydrogenase or quinone oxidoreductase (NADPH:quinone reductase) or alginate lyase
3326	6825	3206646	3206756	111						
3327	6827	3206849	3208024	1176	sp YDEA_ECOLI	Mycobacterium tuberculosis H37Rv Rv0191 ydeA	26.4	66.3	398	membrane transport protein
3328	6828	3208279	3209454	1176	gp AF234535_1	Corynebacterium melassecola (Corynebacterium glutamicum) ATCC 17965 malE	99.7	99.5	392	malate oxidoreductase [NAD] (malic enzyme)
3329	6829	3211186	3209705	1482	sp GNTK_BACSU	Bacillus subtilis gntK	24.5	53.7	486	gluconokinase or gluconate kinase
3330	6830	3211836	3211246	591	sp VANZ_ENTFC	Enterococcus faecium vanZ	27.8	60.4	169	teicoplanin resistance protein
3331	6831	3212429	3211904	525	sp VANZ_ENTFC	Enterococcus faecium vanZ	27.0	159.0	159	teicoplanin resistance protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
3332	6832	3212588	3213931	1344	sp:MERA_STAAU	Staphylococcus aureus merA	29.9	65.6	448	mercury(II) reductase
3333	6833	3215163	3213934	1230	sp:DADA_ECOLI	Escherichia coli K12 dadA	27.3	54.5	444	D-amino acid dehydrogenase small subunit
3334	6834	3216759	3215257	1503						
3335	6835	3217215	3216886	330						
3336	6836	3217777	3217457	321						
3337	6837	3217993	3218601	609	sp:NOX_THETH	Thermus thermophilus nox	25.8	55.2	194	NAD(P)H nitroreductase
3338	6838	3218777	3219700	924						
3339	6839	3221044	3222495	1452						
3340	6840	3222633	3219778	2856	sp:SYL_BACSU	Bacillus subtilis syl	47.7	68.1	943	leucyl-tRNA synthetase
3341	6841	3222722	3223150	429	sp:YBAN_ECOLI	Escherichia coli K12	40.4	40.4	104	hypothetical membrane protein
3342	6842	3223449	3223089	357	sp:VAPI_BACNO	Dichelobacter nodosus vapI	55.8	81.4	86	virulence-associated protein
3343	6843	3224601	3225374	774						
3344	6844	3224714	3223992	723	gp:SCC54_19	Streptomyces coelicolor SCC54.19	31.6	53.8	247	hypothetical protein
3345	6845	3225554	3224718	837	sp:HPCE_ECOLI	Escherichia coli K12 hpcE	28.5	50.3	298	bifunctional protein (homoprotocatechuate catabolism bifunctional isomerase/decarboxylase) (2-hydroxyhepta-2,4-diene-1,7-dioate isomerase and 5-carboxymethyl-2-oxo-hex 3-ene-1,7dioate decarboxylase)
3346	6846	3226687	3225563	1125	gp:AF173167_1	Pseudomonas alcaligenes xlnE	34.2	64.3	339	gentisate 1,2-dioxygenase or 1-hydroxy-2 naphthoate dioxygenase
3347	6847	3227089	3226910	730	sp:KDGR_ERWCH	Pectobacterium chrysanthemi kdgR	25.3	60.7	229	bacterial regulatory protein, lacI family or pectin degradation repressor protein
3348	6848	3227724	3229079	1356	sp:PCAK_PSEPU	Pseudomonas putida pcaK	27.5	60.8	454	transmembrane transport protein or 4-hydroxybenzoate transporter

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
3349	6849	3229119	3230414	1326	prf 1706191A	Pseudomonas putida	28.2	49.4	476	salicylate hydroxylase
3350	6850	3232304	3231054	1251	sp EAT2_HUMAN	Homo sapiens eat2	25.4	54.4	507	proton/glutamate symporter or excitatory amino acid transporter2
3351	6851	3232596	3233105	510	pir JC2326	Corynebacterium glutamicum AS019 ORF1	99.4	99.4	170	tryptophan-specific permease
3352	6852	3233403	3234956	1554	sp TRPE_BRELA	Brevibacterium lactofermentum trpE	99.2	99.8	515	anthranilate synthase component I
3353	6853	3233420	3233250	171						
3354	6854	3234956	3235579	624	TRPG_BRELA	Brevibacterium lactofermentum trpG	99.0	100.0	208	anthranilate synthase component II
3355	6855	3235602	3236645	1044	sp TRPD_CORGL	Corynebacterium glutamicum ATCC 21850 trpD	99.4	99.4	348	anthranilate phosphoribosyltransferase
3356	6856	3236041	3238062	1422	sp TRPC_BRELA	Brevibacterium lactofermentum trpC	97.3	98.3	474	indole-3-glycerol phosphate synthase (IGPS) and N (5' phosphoribosyl) anthranilate isomerase(PRAI)
3357	6857	3237213	3236518	696						
3358	6858	3238082	3239332	1251	sp TRPB_BRELA	Brevibacterium lactofermentum trpB	97.6	97.9	417	tryptophan synthase beta chain
3359	6859	3239332	3240171	840	sp TRPA_BRELA	Brevibacterium lactofermentum trpA	95.4	96.5	283	tryptophan synthase alpha chain
3360	6860	3241851	3240313	1539	gp SCJ21_17	Streptomyces coelicolor A3(2) SCJ21.17c	66.6	86.8	521	hypothetical membrane protein
3361	6861	3242688	3241879	810	sp PTXA_ECOLI	Escherichia coli K12 ptxA	30.3	71.7	152	PTS system, IIA component or unknown pentitol phosphotransferase enzyme II, A component
3362	6862	3242854	3243759	906	sp NOSF_PSEST	Pseudomonas stutzeri	32.5	63.6	305	ABC transporter ATP-binding protein
3363	6863	3243759	3245342	1584	gp SCH10_12	Streptomyces coelicolor A3(2) SCH10.12	25.2	57.2	547	ABC transporter

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
3364	6864	3245317	3245700	450	sp UCRI_CHLLT	Chlorobium limicola petC	32.5	63.6	305	cytchrome b6-F complex iron-sulfur subunit (Rieske iron-sulfur protein)
3365	6865	3246931	3245822	1110	sp NADO_THEBR	Thermoanaerobacter brockii nadO	33.3	64.3	336	NADH oxidase or NADH-dependent flavin oxidoreductase
3366	6866	3247234	3248205	972	sp YFEH_ECOLI	Escherichia coli K12 yfeH	43.6	74.7	328	hypothetical membrane protein
3367	6867	3248392	3249165	774	gp SCI11_36	Streptomyces coelicolor A3(2) SCI11.36c	34.0	54.6	262	hypothetical protein
3368	6868	3249534	3249187	348	pir A29606	Streptomyces coelicolor Plasmid SCP1 mmr	45.1	79.4	102	bacterial regulatory protein, arsR family or methylenomycin A resistance protein
3369	6869	3249651	3250742	1092	sp NADO_THEBR	Thermoanaerobacter brockii nadO	33.4	64.3	347	NADH oxidase or NADH-dependent flavin oxidoreductase
3370	6870	3250758	3251405	648	sp YMY0_YEAST	Saccharomyces cerevisiae ymyO	31.4	69.5	226	hypothetical protein
3371	6871	3251618	3251466	153						
3372	6872	3251934	3251743	192						
3373	6873	3252300	3252133	168						
3374	6874	3252636	3252316	321						
3375	6875	3252728	3253480	753	sp BUDC_KLETE	Klebsiella terrigena budC	26.9	52.9	238	acetoin(diacetyl) reductase (acetoin dehydrogenase)
3376	6876	3253560	3253739	180	sp YY34_MYCTU	Mycobacterium tuberculosis H37Rv Rv2094c	53.5	84.5	58	hypothetical protein
3377	6877	3255182	3253824	1359	sp DTPT_LACLA	Lactococcus lactis subsp. lactis dtpT	34.5	71.6	469	di-/tripeptide transporter
3378	6878	3255549	3255719	171						
3379	6879	3256298	3255744	555	sp ACRR_ECOLI	Escherichia coli K12 acrR	26.1	50.5	188	bacterial regulatory protein, tetR family
3380	6880	3257373	3256471	903	sp CATA_ACICA	Acinetobacter calcoaceticus catA	31.7	62.2	246	hydroxyquinol 1,2-dioxygenase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
3381	6881	3258491	3257403	1089	sp TCBF_PSESQ	Pseudomonas sp. P51	43.0	75.5	351	maleylacetate reductase
3382	6882	3260084	3258561	1524	sp XYLE_ECOLI	Escherichia coli K12 xylE	31.4	58.3	513	sugar transporter or D-xylose proton symporter (D-xylose transporter)
3383	6883	3261129	3261989	861	sp ICLR_SALTY	Salmonella typhimurium iclR	25.7	60.7	280	bacterial transcriptional regulator or acetate operon repressor
3384	6884	3262145	3263221	1077	sp YDGJ_ECOLI	Escherichia coli K12 ydgJ	27.2	55.7	357	oxidoreductase
3385	6885	3263237	3264115	879	gsp W61761	Listeria innocua strain 4450	25.9	58.2	270	diagnostic fragment protein sequence
3386	6886	3264142	3265146	1005	sp MI2D_BACSU	Sinorhizobium meliloti idhA	26.5	59.6	332	myo inositol 2 dehydrogenase
3387	6887	3265184	3266266	1083	sp STRI_STRGR	Streptomyces griseus strI	34.1	62.4	343	dehydrogenase or myo-inositol 2-dehydrogenase or streptomycin biosynthesis protein
3388	6888	3267062	3271093	4032	pir C70044	Bacillus subtilis yvnB	33.3	62.7	1242	phosphoesterase
3389	6889	3268557	3267913	645						
3390	6890	3269235	3268618	618						
3391	6891	3271392	3272477	1086						
3392	6892	3275231	3274488	744	sp UNC1_CAEEL	Caenorhabditis elegans unc1	28.6	57.3	206	stomatin
3393	6893	3276570	3275602	969						
3394	6894	3281599	3276671	4929	gp MBO18605_3	Mycobacterium bovis BCG RvD1-Rv2024c	58.4	80.2	1660	DEAD box RNA helicase family
3395	6895	3282172	3281666	507	prf 2323363AAM	Mycobacterium leprae u2256k	34.8	61.0	141	hypothetical membrane protein
3396	6896	3282742	3283101	360						
3397	6897	3282940	3282347	600	sp THID_BACSU	Bacillus subtilis thiD	50.4	76.8	125	phosphomethylpyrimidine kinase
3398	6898	3283141	3283383	243	pir F70041	Bacillus subtilis yvgY	46.3	70.1	67	mercuric ion binding protein or heavy-metal-associated domain containing protein
3399	6899	3284309	3283473	837	prf 2501295A	Corynebacterium glutamicum proP	29.9	62.3	297	ectoine/proline uptake protein

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
3400	6900	3285355	3284399	957	sp FECB_ECOLI	Escherichia coli K12 fecB	29.4	60.6	279	iron(III) dicitrate-binding periplasmic protein precursor or iron(III) dicitrate transport system permease protein
3401	6901	3285455	3285576	1122	sp MRF1_SCHPO	Schizosaccharomyces pombe mrf1	27.2	58.0	324	mitochondrial respiratory function protein or zinc-binding dehydrogenase or NADPH quinone oxidoreductase
3402	6902	3286622	3287005	384						
3403	6903	3287297	3287079	219						
3404	6904	3288190	3287393	798	sp THID_BACSU	Bacillus subtilis thiD	46.2	75.5	249	phosphomethylpyrimidine kinase
3405	6905	3288209	3288609	345						
3406	6906	3288685	3288885	201	pir F70041	Bacillus subtilis yvgY	41.8	70.1	67	mercuric ion-binding protein or heavy-metal-associated domain containing protein
3407	6907	3289315	3288971	345	sp AZLD_BACSU	Bacillus subtilis azlD	36.3	65.7	102	branched-chain amino acid transport
3408	6908	3290021	3289311	711	sp AZLC_BACSU	Bacillus subtilis azlD	32.1	67.0	212	branched-chain amino acid transport
3409	6909	3290591	3290025	567	sp YQGE_ECOLI	Escherichia coli K12 yqgE	23.7	56.2	169	hypothetical protein
3410	6910	3291942	3290623	1320	sp CCA_ECOLI	Escherichia coli K12 cca	26.8	51.8	471	tRNA nucleotidyltransferase
3411	6911	3292532	3293497	966	pir E70600	Mycobacterium tuberculosis H37Rv Rv3908	43.6	69.2	234	mutator mutT protein
3412	6912	3292882	3292610	273						
3413	6913	3293497	3296007	2511	pir F70600	Mycobacterium tuberculosis H37Rv Rv3909	25.8	54.3	858	hypothetical membrane protein
3414	6914	3296156	3293404	3249	pir G70600	Mycobacterium tuberculosis H37Rv Rv3910	35.7	60.1	1201	hypothetical membrane protein
3415	6915	3297705	3298428	723						
3416	6916	3299661	3300263	603	sp RPSH_PSEAE	Pseudomonas aeruginosa algU	30.2	60.9	189	RNA polymerase sigma-H factor or sigma-70 factor (ECF subfamily)
3417	6917	3300371	3301321	951	sp TRXB_STRCL	Streptomyces clavuligerus trxB	60.4	82.5	308	thiorecoxin reductase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
3418	6918	3301303	3300119	1185						
3419	6919	3301358	3301729	372	sp THI2_CHLRE	Chlamydomonas reinhardtii thi2	42 0	76 5	119	thioredoxin ch2, M-type
3420	6920	3301755	3302996	1242	sp CWLB_BACSU	Bacillus subtilis cwlB	51 0	75 4	196	N-acetylmuramoyl-L-alanine amidase
3421	6921	3302765	3301989	777						
3422	6922	3303435	3304475	1041						
3423	6923	3303616	3302999	618	pir D70851	Mycobacterium tuberculosis H37Rv Rv3916c	34 4	58 5	212	hypothetical protein
3424	6924	3304787	3303636	1152	sp YGI2_PSEPU	Pseudomonas putida ygi2	37 6	60 5	367	hypothetical protein
3425	6925	3305671	3304835	837	sp YGI1_PSEPU	Mycobacterium tuberculosis H37Rv parB	65 0	78 0	272	partitioning or sporulation protein
3426	6926	3306532	3305864	669	sp GIDB_ECOLI	Escherichia coli K12 gidB	36 0	64 7	153	glucose inhibited division protein B
3427	6927	3307632	3306682	951	pir A70852	Mycobacterium tuberculosis H37Rv Rv3921c	44 7	75 4	313	hypothetical membrane protein
3428	6928	3308369	3307971	399	sp RNPA_BACSU	Bacillus subtilis rnpA	26 8	59 4	123	ribonuclease P protein component
3429	6929	3308747	3308412	336	gp MAU19185_1	Mycobacterium avium rplM	83 0	93 6	47	50S ribosomal protein L34
3430	6930	3309028	3309321	294						
3431	6931	3309043	3308822	222						
3432	6932	147980	147573	408	gp AF116184_1	Corynebacterium glutamicum panD	100 0	100 0	136	L-aspartate-alpha-decarboxylase precursor
3433	6933	268001	266154	1848	sp LEU1_CORGL	Corynebacterium glutamicum ATCC 13032 leuA	100 0	100 0	616	2-isopropylmalate synthase
3434	6934	269068	268814	255	sp YLEU_CORGL	Corynebacterium glutamicum (Brevibacterium flavum) ATCC 13032 orfX	100 0	100 0	85	hypothetical protein
3435	6935	270660	271691	1032	sp DHAS_CORGL	Corynebacterium glutamicum asd	100 0	100 0	344	aspartate-semialdehyde dehydrogenase
3436	6936	446075	446521	447	gp AF124518_1	Corynebacterium glutamicum ASO19 aroD	100 0	100 0	149	3-dehydroquinase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
3437	6937	526376	527563	1188	sp EFTU_CORGL	Corynebacterium glutamicum ATCC 13059 tuf	100.0	100.0	396	elongation factor Tu
3438	6938	569452	570771	1320	sp SECY_CORGL	Corynebacterium glutamicum (Brevibacterium flavum) MJ233 secY	100.0	100.0	440	preprotein translocase secY subunit
3439	6939	680044	677831	2214	sp IDH_CORGL	Corynebacterium glutamicum ATCC 13032 icd	100.0	100.0	738	isocitrate dehydrogenase (oxalosuccinatedecarboxylase)
3440	6940	720352	718580	1773	prf 2223173A	Corynebacterium glutamicum ATCC 13032 accBC	100.0	100.0	591	acyl-CoA carboxylase or biotin-binding protein
3441	6941	877838	879148	1311	sp CISY_CORGL	Corynebacterium glutamicum ATCC 13032 gltA	100.0	100.0	437	citrate synthase
3442	6942	879276	879629	354	sp FKBP_CORGL	Corynebacterium glutamicum ATCC 13032 fkbA	100.0	100.0	118	putative binding protein or peptidyl-prolyl cis-trans isomerase
3443	6943	944996	946780	1785	sp BETP_CORGL	Corynebacterium glutamicum ATCC 13032 betP	100.0	100.0	595	glycine betaine transporter
3444	6944	1030283	1029006	1278	sp YLI2_CORGL	Corynebacterium glutamicum ATCC 13032 orf2	100.0	100.0	426	hypothetical membrane protein
3445	6945	1031871	1030369	1503	sp LYSI_CORGL	Corynebacterium glutamicum ATCC 13032 lysI	100.0	100.0	501	L-lysine permease
3446	6946	1154683	1153235	1389	sp AROP_CORGL	Corynebacterium glutamicum ATCC 13032 aroP	100.0	100.0	463	aromatic amino acid permease
3447	6947	1155676	1154729	948	pir S52753	Corynebacterium glutamicum ATCC 13032 orf3	100.0	100.0	316	hypothetical protein
3448	6948	1155731	1156837	1107	prf 2106301A	Corynebacterium glutamicum ATCC 13032 dapE	100.0	100.0	369	succinyl diaminopimelate desuccinylase
3449	6949	1219602	1218031	1572	gp CGPUTP 1	Corynebacterium glutamicum ATCC 13032 putP	100.0	100.0	524	proline transport system
3450	6950	1238274	1239923	1650	sp SYR_CORGL	Corynebacterium glutamicum AS019 ATCC 13059 argS	100.0	100.0	550	arginyl-tRNA synthetase

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
3451	6951	1239929	1241263	1335	sp DCDA_CORGL	Corynebacterium glutamicum AS019 ATCC 13059 lysA	100 0	100 0	445	diaminopimelate (DAP) decarboxylase (meso-diaminopimelate decarboxylase)
3452	6952	1242507	1243841	1335	sp DHOM_CORGL	Corynebacterium glutamicum ASU19 ATCC 13059 hom	100 0	100 0	445	homoserine dehydrogenase
3453	6953	1243855	1244781	927	sp KHSE_CORGL	Corynebacterium glutamicum AS019 ATCC 13059 thrB	100 0	100 0	309	homoserine kinase
3454	6954	1327617	1328243	627	gsp W37716	Corynebacterium glutamicum R127 orf3	100 0	100 0	216	ion channel subunit
3455	6955	1328953	1328246	708	sp LYSE_CORGL	Corynebacterium glutamicum R127 lysE	100 0	100 0	236	lysine exporter protein
3456	6956	1329015	1329884	870	sp LYSG_CORGL	Corynebacterium glutamicum R127 lysG	100.0	100 0	290	lysine export regulator protein
3457	6957	1338131	1340008	1878	sp ILVB_CORGL	Corynebacterium glutamicum ATCC 13032 ilvB	100.0	100 0	626	acetohydroxy acid synthase, large subunit
3458	6958	1340025	1340540	516	pir B48648	Corynebacterium glutamicum ATCC 13032 ilvN	100 0	100 0	172	acetohydroxy acid synthase, small subunit
3459	6959	1340724	1341737	1014	pir C48648	Corynebacterium glutamicum ATCC 13032 ilvC	100 0	100 0	338	acetohydroxy acid isomeroreductase
3460	6960	1353489	1354508	1020	sp LEU3_CORGL	Corynebacterium glutamicum ATCC 13032 leuB	100 0	100 0	340	3 isopropylmalate dehydrogenase
3461	6961	1423217	1425265	2049	prf 2014259A	Corynebacterium glutamicum KCTC1445 ptsM	100.0	100 0	683	PTS system, phosphoenolpyruvate sugar phosphotransferase (mannose and glucose transport)
3462	6962	1466491	1467372	882	sp ARGB_CORGL	Corynebacterium glutamicum ATCC 13032 argB	100 0	100 0	294	acetylglutamate kinase
3463	6963	1468565	1469521	957	sp OTCA_CORGI	Corynebacterium glutamicum ATCC 13032 argF	100 0	100 0	319	ornithine carbamoyltransferase
3464	6964	1469529	1470040	513	gp AF041436_1	Corynebacterium glutamicum ASO19 argR	100 0	100 0	171	arginine represson

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
3465	6965	1544554	1543154	1401	gp CGL238250_1	Corynebacterium glutamicum ATCC 13032 ndh	100.0	100.0	467	NADH dehydrogenase
3466	6966	1586725	1586465	261	gp AF086704_1	Corynebacterium glutamicum ASO19 hisE	100.0	100.0	87	phosphoribosyl-ATP-pyrophosphohydrolase
3467	6967	1675208	1674123	1086	gp CGL007732_4	Corynebacterium glutamicum ATCC 13032 ocd	100.0	100.0	362	ornithine-cyclodecarboxylase
3468	6968	1676623	1675268	1356	gp CGL007732_3	Corynebacterium glutamicum ATCC 13032 amt	100.0	100.0	452	ammonium uptake protein, high affinity
3469	6969	1677279	1677049	231	gp CGL007732_2	Corynebacterium glutamicum ATCC 13032 secG	100.0	100.0	77	protein-export membrane protein secG
3470	6970	1680143	1677387	2757	prf 1509267A	Corynebacterium glutamicum ATCC 13032 ppc	100.0	100.0	919	phosphoenolpyruvate carboxylase
3471	6971	1720898	1719669	1230	gp AF124600_1	Corynebacterium glutamicum AS019 aroC	100.0	100.0	410	chorismate synthase (5-enolpyruvylshikimate-3-phosphate phospholyase)
3472	6972	1880490	1882385	1896	pir B55225	Corynebacterium glutamicum ATCC 13032 cglIIR	100.0	100.0	632	restriction endonuclease
3473	6973	2020854	2021846	993	prf 2204286D	Corynebacterium glutamicum ATCC 13869 sigB	100.0	100.0	331	sigma factor of RNA polymerase transcription factor
3474	6974	2060620	2061504	885	sp GLUB_CORGL	Corynebacterium glutamicum ATCC 13032 gluB	100.0	100.0	295	glutamate-binding protein
3475	6975	2065116	2063989	1128	sp RECA_CORGL	Corynebacterium glutamicum AS019 recA	100.0	100.0	376	recA protein
3476	6976	2080183	2079281	903	sp DAPA_BRELA	Corynebacterium glutamicum (Brevibacterium lactofermentum) ATCC 13869 dapA	100.0	100.0	301	dihydrodipicolinate synthase
3477	6977	2081934	2081191	744	sp DAPB_CORGL	Corynebacterium glutamicum (Brevibacterium lactofermentum) ATCC 13869 dapB	100.0	100.0	248	dihydrodipicolinate reductase
3478	6978	2115363	2113864	1500	gp CGA224946_1	Corynebacterium glutamicum R127 mqo	100.0	100.0	500	L-malate dehydrogenase (acceptor)

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a a)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a a)	Function
3479	6979	2171741	2169666	2076	gp CAJ10319_4	Corynebacterium glutamicum ATCC 13032 glnD	100.0	100.0	692	uridilylyltransferase, uridilylyl-removing enzyme
3480	6980	2172086	2171751	336	gp CAJ10319_3	Corynebacterium glutamicum ATCC 13032 glnB	100.0	100.0	112	nitrogen regulatory protein P-II
3481	6981	2173467	2172154	1314	gp CAJ10319_2	Corynebacterium glutamicum ATCC 13032 amtP	100.0	100.0	438	ammonium transporter
3482	6982	2196082	2194742	1341	pir S32227	Corynebacterium glutamicum ATCC 17965 gdhA	100.0	100.0	447	glutamate dehydrogenase (NADP+)
3483	6983	2207092	2205668	1425	sp KPYK_CORGL	Corynebacterium glutamicum AS019 pyk	100.0	100.0	475	pyruvate kinase
3484	6984	2317550	2316582	969	gp AF096280_1	Corynebacterium glutamicum ATCC 13032 glk	100.0	100.0	323	glucokinase
3485	6985	2348839	2350269	1431	pir S32244A	Corynebacterium glutamicum ATCC 13032 glnA	100.0	100.0	477	glutamine synthetase
3486	6986	2355042	2353600	1443	sp THRC_CORGL	Corynebacterium glutamicum thrC	100.0	100.0	481	threonine synthase
3487	6987	2450172	2448328	1845	pir S01205B	Corynebacterium glutamicum ATCC 13032 ectP	100.0	100.0	615	ectoine/proline/glycine betaine carrier
3488	6988	2470141	2467925	2217	pir I40715	Corynebacterium glutamicum ATCC 13032 aceB	100.0	100.0	739	malate synthase
3489	6989	2474040	2472035	1296	pir I40713	Corynebacterium glutamicum ATCC 13032 aceA	100.0	100.0	432	isocitrate lyase
3490	6990	2497776	2496670	1107	sp PROB_CORGL	Corynebacterium glutamicum ATCC 17965 proB	100.0	100.0	369	glutamate 5-kinase
3491	6991	2591469	2590312	1158	gp AF126953_1	Corynebacterium glutamicum AS019 metB	100.0	100.0	386	cystathionine gamma-synthase
3492	6992	2680127	2679684	444	gp AF112535_2	Corynebacterium glutamicum ATCC 13032 nrdI	100.0	100.0	148	ribonucleotide reductase
3493	6993	2680640	2680410	231	gp AF112535_1	Corynebacterium glutamicum ATCC 13032 nrdH	100.0	100.0	77	glutaredoxin

Table 1 (continued)

SEQ NO (DNA)	SEQ NO (a.a.)	Initial (nt)	Terminal (nt)	ORF (bp)	db Match	Homologous gene	Identity (%)	Similarity (%)	Matched length (a.a.)	Function
3494	6994	2787715	2786756	960	sp DDH_CORGL	Corynebacterium glutamicum KY10755 ddh	100.0	100.0	320	meso-diaminopimelate D-dehydrogenase
3495	6995	2888078	2887944	135	gp CGL238703_1	Corynebacterium glutamicum MH20-22B porA	100.0	100.0	45	porin or cell wall channel forming protein
3496	6996	2936505	2935315	1191	sp ACKA_CORGL	Corynebacterium glutamicum ATCC 13032 ackA	100.0	100.0	397	acetate kinase
3497	6997	2937494	2936508	987	prf 2516394A	Corynebacterium glutamicum ATCC 13032 pta	100.0	100.0	329	phosphate acetyltransferase
3498	6998	2961342	2962718	1377	prf 2309322A	Corynebacterium glutamicum ATCC 13032 cmr	100.0	100.0	459	multidrug resistance protein or macrolide-efflux pump or drug proton antiporter
3499	6999	2966161	2963606	2556	sp CLPB_CORGL	Corynebacterium glutamicum ATCC 13032 clpB	100.0	100.0	852	ATP-dependent protease regulatory subunit
3500	7000	3099522	3098578	945	prf 1210266A	Corynebacterium glutamicum pheA	100.0	100.0	315	prephenate dehydratase
3501	7001	3274074	3272563	1512	prf 2501295A	Corynebacterium glutamicum ATCC 13032 proP	100.0	100.0	504	ectoine/proline uptake protein

Example 2

Determination of effective mutation site

(1) Identification of mutation site based on the comparison of the gene nucleotide sequence of lysine-producing B-6 strain with that of wild type strain ATCC 13032

[0374] *Corynebacterium glutamicum* B-6, which is resistant to S-(2-aminoethyl)cysteine (AEC), rifampicin, streptomycin and 6-azauracil, is a lysine-producing mutant having been mutated and bred by subjecting the wild type ATCC 13032 strain to multiple rounds of random mutagenesis with a mutagen, N-methyl-N'-nitro-N-nitrosoguanidine (NTG) and screening (*Appl. Microbiol.* Biotechnol., *32* 269-273 (1989)). First, the nucleotide sequences of genes derived from the B-6 strain and considered to relate to the lysine production were determined by a method similar to the above. The genes relating to the lysine production include *lysE* and *lysG* which are lysine-excreting genes; *ddh*, *dapA*, *hom* and *lysC* (encoding diaminopimelate dehydrogenase, dihydropicolinate synthase, homoserine dehydrogenase and aspartokinase, respectively) which are lysine-biosynthetic genes; and *pyc* and *zwf* (encoding pyruvate carboxylase and glucose-6-phosphate dehydrogenase, respectively) which are glucose-metabolizing genes. The nucleotide sequences of the genes derived from the production strain were compared with the corresponding nucleotide sequences of the ATCC 13032 strain genome represented by SEQ ID NOS:1 to 3501 and analyzed. As a result, mutation points were observed in many genes. For example, no mutation site was observed in *lysE*, *lysG*, *ddh*, *dapA*, and the like, whereas amino acid replacement mutations were found in *hom*, *lysC*, *pyc*, *zwf*, and the like. Among these mutation points, those which are considered to contribute to the production were extracted on the basis of known biochemical or genetic information. Among the mutation points thus extracted, a mutation, Val59Ala, in *hom* and a mutation, Pro458Ser, in *pyc* were evaluated whether or not the mutations were effective according to the following method.

(2) Evaluation of mutation, Val59Ala, in *hom* and mutation, Pro458Ser, in *pyc*

[0375] It is known that a mutation in hom inducing requirement or partial requirement for homoserine imparts lysine productivity to a wild type strain (*Amino Acid Fermentation*, ed. by Hiroshi Aida *et al.*, Japan Scientific Societies Press). However, the relationship between the mutation, Val59Ala, in *hom* and lysine production is not known. It can be examined whether or not the mutation, Val59Ala, in *hom* is an effective mutation by introducing the mutation to the wild type strain and examining the lysine productivity of the resulting strain. On the other hand, it can be examined whether or not the mutation, Pro458Ser, in *pyc* is effective by introducing this mutation into a lysine-producing strain which has a deregulated lysine-bioxynthetic pathway and is free from the *pyc* mutation, and comparing the lysine productivity of the resulting strain with the parent strain. As such a lysine-producing bacterium, No. 58 strain (FERM BP-7134) was selected (hereinafter referred to the "lysine-producing No. 58 strain" or the "No. 58 strain"). Based on the above, it was determined that the mutation, Val59Ala, in *hom* and the mutation, Pro458Ser, in *pyc* were introduced into the wild type strain of *Corynebacterium glutamicum* ATCC 13032 (hereinafter referred to as the "wild type ATCC 13032 strain" or the "ATCC 13032 strain") and the lysine-producing No. 58 strain, respectively, using the gene replacement method. A plasmid vector pCES30 for the gene replacement for the introduction was constructed by the following method.

[0376] A plasmid vector pCE53 having a kanamycin-resistant gene and being capable of autonomously replicating in Coryneform bacteria (*Mol. Gen. Genet., 196*: 175-178 (1984)) and a plasmid pMOB3 (ATCC 77282) containing a levansucrase gene (*sacB*) of *Bacillus subtilis* (*Molecular Microbiology, 6*: 1195-1204 (1992)) were each digested with *Pst*I. Then, after agarose gel electrophoresis, a pCE53 fragment and a 2.6 kb DNA fragment containing *sacB* were each extracted and purified using GENECLEAN Kit (manufactured by BIO 101). The pCE53 fragment and the 2.6 kb DNA fragment were ligated using Ligation Kit ver. 2 (manufactured by Takara Shuzo), introduced into the ATCC 13032 strain by the electroporation method (*FEMS Microbiology Letters*, 65: 299 (1989)), and cultured on BYG agar medium (medium prepared by adding 10 g of glucose, 20 g of peptone (manufactured by Kyokuto Pharmaceutical), 5 g of yeast extract (manufactured by Difco), and 16 g of Bactoagar (manufactured by Difco) to 1 liter of water, and adjusting its pH to 7.2) containing 25 μg/ml kanamycin at 30°C for 2 days to obtain a transformant acquiring kanamycin-resistance. As a result of digestion analysis with restriction enzymes, it was confirmed that a plasmid extracted from the resulting transformant by the alkali SDS method had a structure in which the 2.6 kb DNA fragment had been inserted into the *Pst*I site of pCE53. This plasmid was named pCES30.

[0377] Next, two genes having a mutation point, *hom* and *pyc*, were amplified by PCR, and inserted into pCES30 according to the TA cloning method (Bio Experiment Illustrated vol. 3, published by Shujunsha). Specifically, pCES30 was digested with *Bam*HI (manufactured by Takara Shuzo), subjected to an agarose gel electrophoresis, and extracted and purified using GENECLEAN Kit (manufactured by BIO 101). The both ends of the resulting pCES30 fragment were blunted with DNA Blunting Kit (manufactured by Takara Shuzo) according to the attached protocol. The blunt-ended pCES30 fragment was concentrated by extraction with phenol/chloroform and precipitation with ethanol, and allowed

to react in the presence of Taq polymerase (manufactured by Roche Diagnostics) and dTTP at 70°C for 2 hours so that a nucleotide, thymine (T), was added to the 3'-end to prepare a T vector of pCES30.

[0378] Separately, chromosomal DNA was prepared from the lysine-producing B-6 strain according to the method of Saito et al. (*Biochem. Biophys. Acta, 72*: 619 (1963)). Using the chromosomal DNA as a template, PCR was carried out with Pfu turbo DNA polymelase (manufactured by Stratagene). In the mutated *hom* gene, the DNAs having the nucleotide sequences represented by SEQ ID NOS:7002 and 7003 were used as the primer set. In the mutated *pyc* gene, the DNAs having the nucleotide sequences represented by SEQ ID NOS:7004 and 7005 were used as the primer set. The resulting PCR product was subjected to agarose gel electrophoresis, and extracted and purified using GENECLEAN Kit (manufactured by BIO 101). Then, the PCR product was allowed to react in the presence of Taq polymerase (manufactured by Roche Diagnostics) and dATP at 72°C for 10 minutes so that a nucleotide, adenine (A), was added to the 3'-end.

[0379] The above pCES30 T vector fragment and the mutated *hom* gene (1.7 kb) or mutated *pyc* gene (3.6 kb) to which the nucleotide A had been added of the PCR product were concentrated by extraction with phenol/chloroform and precipitation with ethanol, and then ligated using Ligation Kit ver. 2. The ligation products were introduced into the ATCC 13032 strain according to the electroporation method, and cultured on BYG agar medium containing 25 μg/ml kanamycin at 30°C for 2 days to obtain kanamycin-resistant transformants. Each of the resulting transformants was cultured overnight in BYG liquid medium containing 25 μg/ml kanamycin, and a plasmid was extracted from the culturing solution medium according to the alkali SDS method. As a result of digestion analysis using restriction enzymes, it was confirmed that the plasmid had a structure in which the 1.7 kb or 3.6 kb DNA fragment had been inserted into pCES30. The plasmids thus constructed were named respectively pChom59 and pCpyc458.

[0380] The introduction of the mutations to the wild type ATCC 13032 strain and the lysine-producing No. 58 strain according to the gene replacement method was carried out according to the following method. Specifically, pChom59 and pCpyc458 were introduced to the ATCC 13032 strain and the No. 58 strain, respectively, and strains in which the plasmid is integrated into the chromosomal DNA by homologous recombination were selected using the method of Ikeda *et al. (Microbiology 144*: 1863 (1998)). Then, the stains in which the second homologous recombination was carried out were selected by a selection method, making use of the fact that the *Bacillus subtilis* levansucrase encoded by pCES30 produced a suicidal substance (*J. of Bacteriol., 174*: 5462 (1992)). Among the selected strains, strains in which the wild type *hom* and *pyc* genes possessed by the ATCC 13032 strain and the No. 58 strain were replaced with the mutated *hom* and *pyc* genes respectively, were isolated. The method is specifically explained below.

[0381] One strain was selected from the transformants containing the plasmid, pChom59 or pCpyc458, and the selected strain was cultured in BYG medium containing 20 μg/ml kanamycin, and pCG11 (Japanese Published Examined Patent Application No. 91827/94) was introduced thereinto by the electroporation method. pCG11 is a plasmid vector having a spectinomycin-resistant gene and a replication origin which is the same as pCE53. After introduction of the pCG11, the strain was cultured on BYG agar medium containing 20 μg/ml kanamycin and 100 μg/ml spectinomycin at 30°C for 2 days to obtain both the kanamycin- and spectinomycin-resistant transformant. The chromosome of one strain of these transformants was examined by the Southern blotting hybridization according to the method reported by Ikeda *et al.* (*Microbiology, 144*: 1863 (1998)). As a result, it was confirmed that pChom59 or pCpyc458 had been integrated into the chromosome by the homologous recombination of the Cambell type. In such a strain, the wild type and mutated *hom* or *pyc* genes are present closely on the chromosome, and the second homologous recombination is liable to arise therebetween.

[0382] Each of these transformants (having been recombined once) was spread on Suc agar medium (medium prepared by adding 100 g of sucrose, 7 g of meat extract, 10 g of peptone, 3 g of sodium chloride, 5 g of yeast extract (manufactured by Difco), and 18 g of Bactoagar (manufactured by Difco) to 1 liter of water, and adjusting its pH 7.2) and cultured at 30°C for a day. Then the colonies thus growing were selected in each case. Since a strain in which the *sacB* gene is present converts sucrose into a suicide substrate, it cannot grow in this medium (*J. Bacteriol., 174*: 5462 (1992)). On the other hand, a strain in which the *sacB* gene was deleted due to the second homologous recombination between the wild type and the mutated *hom* or *pyc* genes positioned closely to each other forms no suicide substrate and, therefore, can grow in this medium. In the homologous recombination, either the wild type gene or the mutated gene is deleted together with the *sacB* gene. When the wild type is deleted together with the *sacB* gene, the gene replacement into the mutated type arises.

[0383] Chromosomal DNA of each the thus obtained second recombinants was prepared by the above method of Saito *et al.* PCR was carried out using Pfu turbo DNA polymerase (manufactured by Stratagene) and the attached buffer. In the *hom* gene, DNAs having the nucleotide sequences represented by SEQ ID NOS:7002 and 7003 were used as the primer set. Also, in the *pyc* gene was used, DNAs having the nucleotide sequences represented by SEQ ID NOS:7004 and 7005 were used as the primer set. The nucleotide sequences of the PCR products were determined by the conventional method so that it was judged whether the *hom* or *pyc* gene of the second recombinant was a wild type or a mutant. As a result, the second recombinant which were called HD-1 and No. 58pyc were target strains having the mutated *hom* gene and *pyc* gene, respectively.

(3) Lysine production test of HD-1 and No. 58pyc strains

[0384] The HD-1 strain (strain obtained by incorporating the mutation, Val59Ala, in the *hom* gene into the ATCC 13032 strain) and the No. 58pyc strain (strain obtained by incorporating the mutation, Pro458Ser, in the *pyc* gene into the lysine-producing No. 58 strain) were subjected to a culture test in a 5 l jar fermenter by using the ATCC 13032 strain and the lysine-producing No. 58 strain respectively as a control. Thus lysine production was examined.

[0385] After culturing on BYG agar medium at 30°C for 24 hours, each strain was inoculated into 250 ml of a seed medium (medium prepared by adding 50 g of sucrose, 40 g of corn steep liquor, 8.3 g of ammonium sulfate, 1 g of urea, 2 g of potassium dihydrogenphosphate, 0.83 g of magnesium sulfate heptahydrate, 10 mg of iron sulfate heptahydrate, 1 mg of copper sulfate pentahydrate, 10 mg of zinc sulfate heptahydrate, 10 mg of β-alanine, 5 mg of nicotinic acid, 1.5 mg of thiamin hydrochloride, and 0.5 mg of biotin to 1 liter of water, and adjusting its pH to 7.2, then to which 30 g of calcium carbonate had been added) contained in a 2 l buffle-attached Erlenmeyer flask and cultured therein at 30°C for 12 to 16 hours. A total amount of the seed culturing medium was inoculated into 1,400 ml of a main culture medium (medium prepared by adding 60 g of glucose, 20 g of corn steep liquor, 25 g of ammonium chloride, 2.5 g of potassium dihydrogenphosphate, 0.75 g of magnesium sulfate heptahydrate, 50 mg of iron sulfate heptahydrate, 13 mg of manganese sulfate pentahydrate, 50 mg of calcium chloride, 6.3 mg of copper sulfate pentahydrate, 1.3 mg of zinc sulfate heptahydrate, 5 mg of nickel chloride hexahydrate, 1.3 mg of cobalt chloride hexahydrate, 1.3 mg of ammonium molybdenate tetrahydrate, 14 mg of nicotinic acid, 23 mg of β-alanine, 7 mg of thiamin hydrochloride, and 0.42 mg of biotin to 1 liter of water) contained in a 5 l jar fermenter and cultured therein at 32°C, 1 vvm and 800 rpm while controlling the pH to 7.0 with aqueous ammonia. When glucose in the medium had been consumed, a glucose feeding solution (medium prepared by adding 400 g glucose and 45 g of ammonium chloride to 1 liter of water) was continuously added. The addition of feeding solution was carried out at a controlled speed so as to maintain the dissolved oxygen concentration within a range of 0.5 to 3 ppm. After culturing for 29 hours, the culture was terminated. The cells were separated from the culture medium by centrifugation and then L-lysine hydrochloride in the supernatant was quantified by high performance liquid chromatography (HPLC). The results are shown in Table 2 below.

Table 2

Strain	L-Lysine hydrochloride yield (g/l)
ATCC 13032	0
HD-1	8
No. 58	45
No. 58pyc	51

[0386] As is apparent from the results shown in Table 2, the lysine productivity was improved by introducing the mutation, Val59Ala, in the *hom* gene or the mutation, Pro458Ser, in the pyc gene. Accordingly, it was found that the mutations are both effective mutations relating to the production of lysine. Strain, AHP-3, in which the mutation, Val59Ala, in the *hom* gene and the mutation, Pro458Ser, in the *pyc* gene have been introduced into the wild type ATCC 13032 strain together with the mutation, Thr331Ile in the *lysC* gene has been deposited on December 5, 2000, in National Institute of Bioscience and Human Technology, Agency of Industrial Science and Technology (Higashi 1-1-3, Tsukuba-shi, Ibaraki, Japan) as FERM BP-7382.

Example 3

Reconstruction of lysine-producing strain based on genome information

[0387] The lysine-producing mutant B-6 strain (*Appl. Microbiol. Biotechnol., 32*: 269-273 (1989)), which has been constructed by multiple round random mutagenesis with NTG and screening from the wild type ATCC 13032 strain, produces a remarkably large amount of lysine hydrochloride when cultured in a jar at 32°C using glucose as a carbon source. However, since the fermentation period is long, the production rate is less than 2.1 g/l/h. Breeding to reconstitute only effective mutations relating to the production of lysine among the estimated at least 300 mutations introduced into the B-6 strain in the wild type ATCC 13032 strain was performed.

(1) Identification of mutation point and effective mutation by comparing the gene nucleotide sequence of the B-6 strain with that of the ATCC 13032 strain

[0388] As described above, the nucleotide sequences of genes derived from the B-6 strain were compared with the

corresponding nucleotide sequences of the ATCC 13032 strain genome represented by SEQ ID NOS:1 to 3501 and analyzed to identify many mutation points accumulated in the chromosome of the B-6 strain. Among these, a mutation, Val591Ala, in *hom*, a mutation, Thr311Ile, in *lysC*, a mutation, Pro458Ser, in *pyc* and a mutation, Ala213Thr, in *zwf* were specified as effective mutations relating to the production of lysine. Breeding to reconstitute the 4 mutations in the wild type strain and for constructing of an industrially important lysine-producing strain was carried out according to the method shown below.

(2) Construction of plasmid for gene replacement having mutated gene

[0389] The plasmid for gene replacement, pChom59, having the mutated *hom* gene and the plasmid for gene replacement, pCpyc458, having the mutated *pyc* gene were prepared in the above Example 2(2). Plasmids for gene replacement having the mutated *lysC* and *zwf* were produced as described below.

[0390] The *lysC* and *zwf* having mutation points were amplified by PCR, and inserted into a plasmid for gene replacement, pCES30, according to the TA cloning method described in Example 2(2) (Bio Experiment Illustrated, Vol. 3).

[0391] Separately, chromosomal DNA was prepared from the lysine-producing B-6 strain according to the above method of Saito *et al.* Using the chromosomal DNA as a template, PCR was carried out with Pfu turbo DNA polymerase (manufactured by Stratagene). In the mutated *lysC* gene, the DNAs having the nucleotide sequences represented by SEQ ID NOS:7006 and 7007 were used as the primer set. In the mutated *zwf* gene, the DNAs having the nucleotide sequences represented by SEQ ID NOS:7008 and 7009 as the primer set. The resulting PCR product was subjected to agarose gel electrophoresis, and extracted and purified using GENEGLEAN Kit (manufactured by BIO 101). Then, the PCR product was allowed to react in the presence of Taq DNA polymerase (manufactured by Roche Diagnostics) and dATP at 72°C for 10 minutes so that a nucleotide, adenine (A), was added to the 3'-end.

[0392] The above pCES30 T vector fragment and the mutated *lysC* gene (1.5 kb) or mutated *zwf* gene (2.3 kb) to which the nucleotide A had been added of the PCR product were concentrated by extraction with phenol/chloroform and precipitation with ethanol, and then ligated using Ligation Kit ver. 2. The ligation products were introduced into the ATCC 13032 strain according to the electroporation method, and cultured on BYG agar medium containing 25 μg/ml kanamycin at 30°C for 2 days to obtain kanamycin-resistant transformants. Each of the resulting transformants was cultured overnight in BYG liquid medium containing 25 μg/ml kanamycin, and a plasmid was extracted from the culturing solution medium according to the alkali SDS method. As a result of digestion analysis using restriction enzymes, it was confirmed that the plasmid had a structure in which the 1.5 kb or 2.3 kb DNA fragment had been inserted into pCES30. The plasmids thus constructed were named respectively pClysC311 and pCzwf213.

(3) Introduction of mutation, Thr311Ile, in *lysC* into one point mutant HD-1

[0393] Since the one mutation point mutant HD-1 in which the mutation, Val59Ala, in *hom* was introduced into the wild type ATCC 13032 strain had been obtained in Example 2(2), the mutation, Thr311Ile, in *lysC* was introduced into the HD-1 strain using pClysC311 produced in the above (2) according to the gene replacement method described in Example 2(2). PCR was carried out using chromosomal DNA of the resulting strain and, as the primer set, DNAs having the nucleotide sequences represented by SEQ ID NOS:7006 and 7007 in the same manner as in Example 2(2). As a result of the fact that the nucleotide sequence of the PCR product was determined in the usual manner, it was confirmed that the strain which was named AHD-2 was a two point mutant having the mutated *lysC* gene in addition to the mutated *hom* gene.

(4) Introduction of mutation, Pro458Ser, in *pyc* into two point mutant AHD-2

[0394] The mutation, Pro458Ser, in *pyc* was introduced into the AHD-2 strain using the pCpyc458 produced in Example 2(2) by the gene replacement method described in Example 2(2). PCR was carried out using chromosomal DNA of the resulting strain and, as the primer set, DNAs having the nucleotide sequences represented by SEQ ID NOS:7004 and 7005 in the same manner as in Example 2(2). As a result of the fact that the nucleotide sequence of the PCR product was determined in the usual manner, it was confirmed that the strain which was named AHD-3 was a three point mutant having the mutated *pyc* gene in addition to the mutated *hom* gene and *lysC* gene.

(5) Introduction of mutation, Ala213Thr, in *zwf* into three point mutant AHP-3

[0395] The mutation, Ala213Thr, in *zwf* was introduced into the AHP-3 strain using the pCzwf458 produced in the above (2) by the gene replacement method described in Example 2(2). PCR was carried out using chromosomal DNA of the resulting strain and, as the primer set, DNAs having the nucleotide sequences represented by SEQ ID NOS:7008 and 7009 in the same manner as in Example 2(2). As a result of the fact that the nucleotide sequence of the PCR

product was determined in the usual manner. It was confirmed that the strain which was named APZ-4 was a four point mutant having the mutated *zwf* gene in addition to the mutated *hom* gene, *lysC* gene and *pyc* gene.

(6) Lysine production test on HD-1, AHD-2, AHP-3 and APZ-4 strains

[0396] The HD-1, AHD-2, AHP-3 and APZ-4 strains obtained above were subjected to a culture test in a 5 l jar fermenter in accordance with the method of Example 2(3).

[0397] Table 3 shows the results.

Table 3

Strain	L-Lysine hydrochloride (g/l)	Productivity (g/l/h)
HD-1	8	0.3
AHD-2	73	2.5
AHP-3	80	2.8
APZ-4	86	3.0

[0398] Since the lysine-producing mutant B-6 strain which has been bred based on the random mutation and selection shows a productivity of less than 2.1 g/l/h, the APZ-4 strain showing a high productivity of 3.0 g/l/h is useful in industry.

(7) Lysine fermentation by APZ-4 strain at high temperature

[0399] The APZ-4 strain, which had been reconstructed by introducing 4 effective mutations into the wild type strain, was subjected to the culturing test in a 5 l jar fermenter in the same manner as in Example 2(3), except that the culturing temperature was changed to 40°C.

[0400] The results are shown in Table 4.

Table 4

Temperature (°C)	L-Lysine hydrochloride (g/l)	Productivity (g/l/h)
32	86	3.0
40	95	3.3

[0401] As is apparent from the results shown in Table 4, the lysine hydrochloride titer and productivity in culturing at a high temperature of 40°C comparable to those at 32°C were obtained. In the mutated and bred lysine-producing B-6 strain constructed by repeating random mutation and selection, the growth and the lysine productivity are lowered at temperatures exceeding 34°C so that lysine fermentation cannot be carried out, whereas lysine fermentation can be carried out using the APZ-4 strain at a high temperature of 40°C so that the load of cooling is greatly reduced and it is industrially useful. The lysine fermentation at high temperatures can be achieved by reflecting the high temperature adaptability inherently possessed by the wild type strain on the APZ-4 strain.

[0402] As demonstrated in the reconstruction of the lysine-producing strain, the present invention provides a novel breeding method effective for eliminating the problems in the conventional mutants and acquiring industrially advantageous strains. This methodology which reconstitutes the production strain by reconstituting the effective mutation is an approach which is efficiently carried out using the nucleotide sequence information of the genome disclosed in the present invention, and its effectiveness was found for the first time in the present invention.

Example 4

Production of DNA microarray and use thereof

[0403] A DNA microarray was produced based on the nucleotide sequence information of the ORF deduced from the full nucleotide sequences of *Corynebacterium glutamicum* ATCC 13032 using software, and genes of which expression is fluctuated depending on the carbon source during culturing were searched.

(1) Production of DNA microarray

[0404] Chromosomal DNA was prepared from *Corynebacterium glutamicum* ATCC 13032 by the method of Saito *et*

al. (Biochem. Biophys. Acta, 72: 619 (1963)). Based on 24 genes having the nucleotide sequences represented by SEQ ID NOS:207, 3433, 281, 3435, 3439, 765, 3445, 1226, 1229, 3448, 3451, 3453, 3455, 1743, 3470, 2132, 3476, 3477, 3485, 3488, 3489, 3494, 3496, and 3497 from the ORFs shown in Table 1 deduced from the full genome nucleotide sequence of *Corynebacterium glutamicum* ATCC 13032 using software and the nucleotide sequence of rabbit globin gene (GenBank Accession No. V00882) used as an internal standard, oligo DNA primers for PCR amplification represented by SEQ ID NOS:7010 to 7059 targeting the nucleotide sequences of the genes were synthesized in a usual manner.

[0405] As the oligo DNA primers used for the PCR,

[0406] DNAs having the nucleotide sequence represented by SEQ ID NOS:7010 and 7011 were used for the amplification of the DNA having the nucleotide sequence represented by SEQ ID NO:207.

[0407] DNAs having the nucleotide sequence represented by SEQ ID NOS:7012 and 7013 were used for the amplification of the DNA having the nucleotide sequence represented by SEQ ID NO:3433,

[0408] DNAs having the nucleotide sequence represented by SEQ ID NOS:7014 and 7015 were used for the amplification of the DNA having the nucleotide sequence represented by SEQ ID NO:281,

[0409] DNAs having the nucleotide sequence represented by SEQ ID NOS:7016 and 7017 were used for the amplification of the DNA having the nucleotide sequence represented by SEQ ID NO:3435,

[0410] DNAs having the nucleotide sequence represented by SEQ ID NOS:7018 and 7019 were used for the amplification of the DNA having the nucleotide sequence represented by SEQ ID NO:3439,

[0411] DNAs having the nucleotide sequence represented by SEQ ID NOS:7020 and 7021 were used for the amplification of the DNA having the nucleotide sequence represented by SEQ ID NO:765,

[0412] DNAs having the nucleotide sequence represented by SEQ ID NOS:7022 and 7023 were used for the amplification of the DNA having the nucleotide sequence represented by SEQ ID NO:3445,

[0413] DNAs having the nucleotide sequence represented by SEQ ID NOS:7024 and 7025 were used for the amplification of the DNA having the nucleotide sequence represented by SEQ ID NO:1226,

[0414] DNAs having the nucleotide sequence represented by SEQ ID NOS:7026 and 7027 were used for the amplification of the DNA having the nucleotide sequence represented by SEQ ID NO:1229,

[0415] DNAs having the nucleotide sequence represented by SEQ ID NOS:7028 and 7029 were used for the amplification of the DNA having the nucleotide sequence represented by SEQ ID NO:3448,

[0416] DNAs having the nucleotide sequence represented by SEQ ID NOS:7030 and 7031 were used for the amplification of the DNA having the nucleotide sequence represented by SEQ ID NO:3451,

[0417] DNAs having the nucleotide sequence represented by SEQ ID NOS:7032 and 7033 were used for the amplification of the DNA having the nucleotide sequence represented by SEQ ID NO:3453,

[0418] DNAs having the nucleotide sequence represented by SEQ ID NOS:7034 and 7035 were used for the amplification of the DNA having the nucleotide sequence represented by SEQ ID NO:3455,

[0419] DNAs having the nucleotide sequence represented by SEQ ID NOS:7036 and 7037 were used for the amplification of the DNA having the nucleotide sequence represented by SEQ ID NO:1743,

[0420] DNAs having the nucleotide sequence represented by SEQ ID NOS:7038 and 7039 were used for the amplification of the DNA having the nucleotide sequence represented by SEQ ID NO 3470,

[0421] DNAs having the nucleotide sequence represented by SEQ ID NOS:7040 and 7041 were used for the amplification of the DNA having the nucleotide sequence represented by SEQ ID NO 2132,

[0422] DNAs having the nucleotide sequence represented by SEQ ID NOS:7042 and 7043 were used for the amplification of the DNA having the nucleotide sequence represented by SEQ ID NO:3476,

[0423] DNAs having the nucleotide sequence represented by SEQ ID NOS:7044 and 7045 were used for the amplification of the DNA having the nucleotide sequence represented by SEQ ID NO:3477,

[0424] DNAs having the nucleotide sequence represented by SEQ ID NOS:7046 and 7047 were used for the amplification of the DNA having the nucleotide sequence represented by SEQ ID NO 3485,

[0425] DNAs having the nucleotide sequence represented by SEQ ID NOS:7048 and 7049 were used for the amplification of the DNA having the nucleotide sequence represented by SEQ ID NO 3488,

[0426] DNAs having the nucleotide sequence represented by SEQ ID NOS:7050 and 7051 were used for the amplification of the DNA having the nucleotide sequence represented by SEQ ID NO 3489,

[0427] DNAs having the nucleotide sequence represented by SEQ ID NOS:7052 and 7053 were used for the amplification of the DNA having the nucleotide sequence represented by SEQ ID NO 3494,

[0428] DNAs having the nucleotide sequence represented by SEQ ID NOS:7054 and 7055 were used for the amplification of the DNA having the nucleotide sequence represented by SEQ ID NO:3496,

[0429] DNAs having the nucleotide sequence represented by SEQ ID NOS:7056 and 7057 were used for the amplification of the DNA having the nucleotide sequence represented by SEQ ID NO:3497, and

[0430] DNAs having the nucleotide sequence represented by SEQ ID NOS:7058 and 7059 were used for the amplification of the DNA having the nucleotide sequence of the rabbit globin gene.

as the respective primer set

[0431] The PCR was carried for 30 cycles with each cycle consisting of 15 seconds at 95°C and 3 minutes at 68°C using a thermal cycler (GeneAmp PCR system 9600, manufactured by Perkin Elmer) TaKaRa EX-Taq (manufactured by Takara Shuzo). 100 ng of the chromosomal DNA and the buffer attached to the TaKaRa Ex-Taq reagent. In the case of the rabbit globin gene, a single-stranded cDNA which had been synthesized from rabbit globin mRNA (manufactured by Life Technologies) according to the manufacture's instructions using a reverse transcriptase RAV-2 (manufactured by Takara Shuzo). The PCR product of each gene thus amplified was subjected to agarose gel electrophoresis and extracted and purified using QIAquick Gel Extraction Kit (manufactured by QIAGEN). The purified PCR product was concentrated by precipitating it with ethanol and adjusted to a concentration of 200 ng/μl. Each PCR product was spotted on a slide glass plate (manufactured by Matsunami Glass) having MAS coating in 2 runs using GTMASS SYSTEM (manufactured by Nippon Laser & Electronics Lab.) according to the manufacture's instructions.

(2) Synthesis of fluorescence labeled cDNA

[0432] The ATCC 13032 strain was spread on BY agar medium (medium prepared by adding 20 g of peptone (manufactured by Kyokuto Pharmaceutical), 5 g of yeast extract (manufactured by Difco), and 16 g of Bactoagar (manufactured by Difco) to in 1 liter of water and adjusting its pH to 7.2) and cultured at 30°C for 2 days. Then, the cultured strain was further inoculated into 5 ml of BY liquid medium and cultured at 30°C overnight. Then, the cultured strain was further inoculated into 30 ml of a minimum medium (medium prepared by adding 5 g of ammonium sulfate, 5 g of urea, 0.5 g of monopotassium dihydrogenphosphate, 0.5 g of dipotassium monohydrogenphosphate, 20.9 g of morpholinopropanesulfonic acid, 0.25 g of magnesium sulfate heptahydrate, 10 mg of calcium chloride dihydrate, 10 mg of manganese sulfate monohydrate, 10 mg of ferrous sulfate heptahydrate, 1 mg of zinc sulfate heptahydrate, 0.2 mg copper sulfate, and 0.2 mg biotin to 1 liter of water, and adjusting its pH to 6.5) containing 110 mmol/l glucose or 200 mmol/l ammonium acetate, and cultured in an Erlenmyer flask at 30° to give 1.0 of absorbance at 660 nm. After the cells were prepared by centrifuging at 4°C and 5,000 rpm for 10 minutes, total RNA was prepared from the resulting cells according to the method of Bormann *et al. (Molecular Microbiology, 6*: 317-326 (1992)). To avoid contamination with DNA, the RNA was treated with DnaseI (manufactured by Takara Shuzo) at 37°C for 30 minutes and then further purified using Qiagen RNeasy MiniKit (manufactured by QIAGEN) according to the manufacture's instructions. To 30 μg of the resulting total RNA, 0.6 μl of rabbit globin mRNA (50 ng/μl, manufactured by Life Technologies) and 1 μl of a random 6 mer primer (500 ng/μl, manufactured by Takara Shuzo) were added for denaturing at 65°C for 10 minutes, followed by quenching on ice. To the resulting solution, 6 μl of a buffer attached to Superscript II (manufactured by Lifetechnologies), 3 μl of 0.1 mol/l DTT, 1.5 μl of dNTPs (25 mmol/l dATP, 25 mmol/l dCTP, 25 mmol/l dGTP, 10 mmol/l dTTP), 1.5 μl of Cy5-dUTP or Cy3-dUTP (manufactured by NEN) and 2 μl of Superscript II were added, and allowed to stand at 25°C for 10 minutes and then at 42°C for 110 minutes. The RNA extracted from the cells using glucose as the carbon source and the RNA extracted from the cells using ammonium acetate were labeled with Cy5-dUTP and Cy3-dUTP, respectively. After the fluorescence labeling reaction, the RNA was digested by adding 1.5 μl of 1 mol/l sodium hydroxide-20 mmol/l EDTA solution and 3.0 μl of 10% SDS solution, and allowed to stand at 65°C for 10 minutes. The two cDNA solutions after the labeling were mixed and purified using Qiagen PCR purification Kit (manufactured by QIAGEN) according to the manufacture's instructions to give a volume of 10 μl.

(3) Hybridization

[0433] UltraHyb (110 μl) (manufactured by Ambion) and the fluorescence-labeled cDNA solution (10 μl) were mixed and subjected to hybridization and the subsequent washing of slide glass using GeneTAC Hybridization Station (manufactured by Genomic Solutions) according to the manufacture's instructions. The hybridization was carried out at 50°C, and the washing was carried out at 25°C

(4) Fluorescence analysis

[0434] The fluorescence amount of each DNA array having the fluorescent cDNA hybridized therewith was measured using ScanArray 4000 (manufactured by GSI Lumonics).

[0435] Table 5 shows the Cy3 and Cy5 signal intensities of the genes having been corrected on the basis of the data of the rabbit globin used as the internal standard and the Cy3/Cy5 ratios.

Table 5

SEQ ID NO	Cy3 intensity	Cy5 intensity	Cy3/Cy5
207	5248	3240	1.62

Table 5 (continued)

SEQ ID NO	Cy3 intensity	Cy5 intensity	Cy3/Cy5
3433	2239	2694	0.83
281	2370	2595	0.91
3435	2566	2515	1.02
3439	5597	6944	0.81
765	6134	4943	1.24
3455	1169	1284	0.91
1226	1301	1493	0.87
1229	1168	1131	1.03
3448	1187	1594	0.74
3451	2845	3859	0.74
3453	3498	1705	2.05
3455	1491	1144	1.30
1743	1972	1841	1.07
3470	4752	3764	1.26
2132	1173	1085	1.08
3476	1847	1420	1.30
3477	1284	1164	1.10
3485	4539	8014	0.57
3488	34289	1398	24.52
3489	43645	1497	29.16
3494	3199	2503	1.28
3496	3428	2364	1.45
3497	3848	3358	1.15

[0436] The ORF function data estimated by using software were searched for SEQ ID NOS:3488 and 3489 showing remarkably strong Cy3 signals. As a result, it was found that SEQ ID NOS:3488 and 3489 are a maleate synthase gene and an isocitrate lyase gene, respectively. It is known that these genes are transcriptionally induced by acetic acid in *Corynebacterium glutamicum* (*Archives of Microbiology, 168*: 262-269 (1997)).

[0437] As described above, a gene of which expression is fluctuates could be discovered by synthesizing appropriate oligo DNA primers based on the ORF nucleotide sequence information deduced from the full genomic nucleotide sequence information of *Corynebacterium glutamicum* ATCC 13032 using software, amplifying the nucleotide sequences of the gene using the genome DNA of *Corynebacterium glutamicum* as a template in the PCR reaction, and thus producing and using a DNA microarray.

[0438] This Example shows that the expression amount can be analyzed using a DNA microarray in the 24 genes. On the other hand, the present DNA microarray techniques make it possible to prepare DNA microarrays having thereon several thousand gene probes at once. Accordingly, it is also possible to prepare DNA microarrays having thereon all of the ORF gene probes deduced from the full genomic nucleotide sequence of *Corynebacterium glutamicum* ATCC 13032 determined by the present invention, and analyze the expression profile at the total gene level of *Corynebacterium glutamicum* using these arrays.

Example 5

Homology search using *Corynebacterium glutamicum* genome sequence

(1) Search of adenosine deaminase

[0439] The amino acid sequence (ADD_ECOLI) of *Escherichia coli* adenosine deaminase was obtained from Swissprot Database as the amino acid sequence of the protein of which function had been confirmed as adenosine deaminase (EC3.5.4.4). By using the full length of this amino acid sequence as a query, a homology search was carried out on a nucleotide sequence database of the genome sequence of *Corynebacterium glutamicum* or a database of the amino acids in the ORF region deduced from the genome sequence using FASTA program (*Proc. Natl. Acad. Sci. USA, 85*: 2444-2448 (1988)). A case where E-value was $1e^{-10}$ or less was judged as being significantly homologous. As a result,

no sequence significantly homologous with the *Escherichia coli* adenosine deaminase was found in the nucleotice sequence database of the genome sequence of *Corynebacterium glutamicum* or the database of the amino acid sequences in the ORF region deduced from the genome sequence. Based on these results, it is assumed that *Corynebacterium glutamicum* contains no ORF having adenosine deaminase activity and thus has no activity of converting adenosine nto inosine.

(2) Search of glycine cleavage enzyme

[0440] The sequences (GCSP_ECOLI, GCST_ECOLI and GCSH_ECOLI) of glycine decarboxylase, aminomethyl transferase and an aminomethyl group carrier each of which is a component of *Escherichia coli* glycine cleavage enzyme as the amino acid sequence of the protein, of which function had been confirmed as glycine cleavage enzyme (EC2.1.2.10), were obtained from Swiss-prot Database.

[0441] By using these full-length amino acid sequences as a query, a nomology search was carried out on a nucleotice sequence database of the genome sequence of *Corynebacterium glutamicum* or a database of the ORF amino acid sequences deduced from the genome sequence using FASTA program. A case where E-value was $1e^{-10}$ or less was judged as being significantly homologous. As a result, no sequence significantly homologous with the glycine decarboxylase, the aminomethyl transferase or the aminomethyl group carrier each of which is a component of *Escherichia coli* glycine cleavage enzyme, was found in the nucleotide sequence database of the genome sequence of *Corynebacterium glutamicum* or the database of the ORF amino acid sequences estimated from the genome sequence. Based on these results, it is assumed that *Corynebacterium glutamicum* contains no ORF having the activity of glycine decarboxylase, aminomethyl transferase or the aminomethyl group carrier and thus has no activity of the glycine cleavage enzyme

(3) Search of IMP dehydrogenase

[0442] The amino acid sequence (IMDH_ECOLI) of *Escherichia coli* IMP dehydrogenase as the amino acid sequence of the protein, of which function had been confirmed as IMP dehydrogenase (EC1.1.1.205), was obtained from Swiss-prot Database. By using the full length of this amino acid sequence as a query, a homology search was carried out on a nucleotide sequence database of the genome sequence of *Corynebacterium glutamicum* or a database of the ORF amino acid sequences predicted from the genome sequence using FASTA program. A case where E-value was $1e^{-10}$ or less was judged as being significantly homologous. As a result, the amino acid sequences encoded by two ORFs, namely, an ORF positioned in the region of the nucleotide sequence No. 615336 to 616853 (or ORF having the nucleotide sequence represented by SEQ ID NO:672) and another ORF positioned in the region of the nucleotide sequence No. 616973 to 618094 (or ORF having the nucleotide sequence represented by SEQ ID NO 674) were significantly homologous with the ORFs of *Escherichia coli* IMP dehydrogenase. By using the above-described predicted amino acid sequence as a query in order to examine the similarity of the amino acid sequences encoded by the ORFs with IMP dehydrogenases of other organisms in greater detail, a search was carried out on GenBank (http://www.ncbi.nlm.nih.gov/) nr-aa database (amino acid sequence database constructed on the basis of GenBankCDS translation products, PDB database, Swiss-Prot database, PIR database, PRF database by eliminating duplicated registrations) using BLAST program. As a result, both of the two amino acid sequences showed significant homologies with IMP dehdyrogenases of other organisms and clearly higher homologies with IMP dehdyrogenases than with amino acid sequences of other proteins, and thus, it was assumed that the two ORFs would function as IMP dehydrogenase. Based on these results, it was therefore assumed that *Corynebacterium glutamicum* has two ORFs having the IMP dehydrogenase activity.

Example 6

Proteome analysis of proteins derived from *Corynebacterium glutamicum*

(1) Preparations of proteins derived from *Corynebacterium glutamicum* ATCC 13032, FERM BP-7134 and FERM BP-158

[0443] Culturing tests of *Corynebacterium glutamicum* ATCC 13032 (wild type strain), *Corynebacterium glutamicum* FERM BP-7134 (lysine-producing strain) and *Corynebacterium glutamicum* (FERM BP-158, lysine-highly producing strain) were carried out in a 5 l jar fermenter according to the method in Example 2(3). The results are shown in Table 6.

Table 6

Strain	L-Lysine yield (g/l)
ATCC 13032	0
FERM BP-7134	45
FERM BP-158	60

[0444] After culturing, cells of each strain were recovered by centrifugation. These cells were washed with Tris-HCl buffer (10 mmol/l Tris-HCl, pH 6.5, 1.6 mg/ml protease inhibitor (COMPLETE; manufactured by Boehringer Mannheim)) three times to give washed cells which could be stored under freezing at -80°C. The freeze-stored cells were thawed before use, and used as washed cells.

[0445] The washed cells described above were suspended in a disruption buffer (10 mmol/l Tris-HCl, pH 7.4, 5 mmol/l magnesium chloride, 50 mg/l RNase, 1.6 mg/ml protease inhibitor (COMPLETE; manufactured by Boehringer Mannheim)), and disrupted with a disruptor (manufactured by Brown) under cooling. To the resulting disruption solution, DNase was added to give a concentration of 50 mg/l, and allowed to stand on ice for 10 minutes. The solution was centrifuged (5,000 × g, 15 minutes, 4°C) to remove the undisrupted cells as the precipitate, and the supernatant was recovered.

[0446] To the supernatant, urea was added to give a concentration of 9 mol/l, and an equivalent amount of a lysis buffer (9.5 mol/l urea, 2% NP-40, 2% Ampholine, 5% mercaptoethanol, 1.6 mg/ml protease inhibitor (COMPLETE; manufactured by Boehringer Mannheim) was added thereto, followed by thoroughly stirring at room temperature for dissolving.

[0447] After being dissolved, the solution was centrifuged at 12,000 × g for 15 minutes, and the supernatant was recovered.

[0448] To the supernatant, ammonium sulfate was added to the extent of 80% saturation, followed by thoroughly stirring for dissolving.

[0449] After being dissolved, the solution was centrifuged (16,000 × g, 20 minutes, 4°C), and the precipitate was recovered. This precipitate was dissolved in the lysis buffer again and used in the subsequent procedures as a protein sample. The protein concentration of this sample was determined by the method for quantifying protein of Bradford.

(2) Separation of protein by two dimensional electrophoresis

[0450] The first dimensional electrophoresis was carried out as described below by the isoelectric electrophoresis method.

[0451] A molded dry IPG strip gel (pH 4-7, 13 cm, Immobiline DryStrips; manufactured by Amersham Pharmacia Biotech) was set in an electrophoretic apparatus (Multiphor II or IPGphor; manufactured by Amersham Pharmacia Biotech) and a swelling solution (8 mol/l urea, 0.5% Triton X-100, 0.6% dithiothreitol, 0.5% Ampholine, pH 3-10) was packed therein, and the gel was allowed to stand for swelling 12 to 16 hours.

[0452] The protein sample prepared above was dissolved in a sample solution (9 mol/l urea, 2% CHAPS, 1% dithiothreitol, 2% Ampholine, pH 3-10), and then about 100 to 500 μg (in terms of protein) portions thereof were taken and added to the swollen IPG strip gel.

[0453] The electrophoresis was carried out in the 4 steps as defined below under controlling the temperature to 20°C:

step 1: 1 hour under a gradient mode of 0 to 500V;
step 2: 1 hour under a gradient mode of 500 to 1,000 V;
step 3: 4 hours under a gradient mode of 1,000 to 8,000 V; and
step 4: 1 hour at a constant voltage of 8,000 V.

[0454] After the isoelectric electrophoresis, the IPG strip gel was put off from the holder and soaked in an equilibration buffer A (50 mmol/l Tris-HCl, pH 6.8, 30% glycerol, 1% SDS, 0.25% dithiothreitol) for 15 minutes and another equilibration buffer B (50 mmol/l Tris-HCl, pH 6.8, 6 mol/l urea, 30% glycerol, 1% SDS, 0.45% iodo acetamide) for 15 minutes to sufficiently equilibrate the gel.

[0455] After the equilibrium, the IPG strip gel was lightly rinsed in an SDS electrophoresis buffer (1.4% glycine, 0.1% SDS, 0.3% Tris-HCl, pH 8.5), and the second dimensional electrophoresis depending on molecular weight was carried out as described below to separate the proteins.

[0456] Specifically, the above IPG strip gel was closely placed on 14% polyacrylamide slub gel (14% polyacrylamide, 0.37% bisacrylamide, 37.5 mmol/l Tris-HCl, pH 8.8, 0.1% SDS, 0.1% TEMED, 0.1% ammonium persulfate) and sub-

jected to electrophoresis under a constant voltage of 30 mA at 20°C for 3 hours to separate the proteins.

(3) Detection of protein spot

[0457] Coomassie staining was performed by the method of Gorg et al. (*Electrophoresis, 9*: 531-546 (1988)) for the slub gel after the second dimensional electrophoresis. Specifically, the slub gel was stained under shaking at 25°C for about 3 hours, the excessive coloration was removed with a decoloring solution, and the gel was thoroughly washed with distilled water.

[0458] The results are shown in Fig. 2. The proteins derived from the ATCC 13032 strain (Fig. 2A) FERM BP-7134 strain (Fig. 2B) and FERM BP-158 strain (Fig. 2C) could be separated and detected as spots.

(4) In-gel digestion of detected protein spot

[0459] The detected spots were each cut out from the gel and transferred into siliconized tube, and 400 μl of 100 mmol/1 ammonium bicarbonate : acetonitrile solution (1:1, v/v) was added thereto, followed by shaking overnight and freeze-dried as such. To the dried gel, 10 μl of a lysylendopeptidase (LysC) solution (manufactured by WAKO, prepared with 0.1% SDS-containing 50 mmol/l ammonium bicarbonate to give a concentration of 100 ng/μl) was added and the gel was allowed to stand for swelling at 0°C for 45 minutes, and then allowed to stand at 37°C for 16 hours. After removing the LysC solution, 20 μl of an extracting solution (a mixture of 60% acetonitrile and 5% formic acid) was added, followed by ultrasonication at room temperature for 5 minutes to disrupt the gel. After the disruption, the extract was recovered by centrifugation (12,000 rpm, 5 minutes, room temperature). This operation was repeated twice to recover the whole extract. The recovered extract was concentrated by centrifugation *in vacuo* to halve the liquid volume. To the concentrate, 20 μl of 0.1% trifluoroacetic acid was added, followed by thoroughly stirring, and the mixture was subjected to desalting using ZipTip (manufactured by Millipore). The protein absorbed on the carriers of ZipTip was eluted with 5 μl of α-cyano-4-hydroxycinnamic acid for use as a sample solution for analysis.

(5) Mass spectrometry and amino acid sequence analysis of protein spot with matrix assisted laser desorption ionization time of flight mass spectrometer (MALDI-TOFMS)

[0460] The sample solution for analysis was mixed in the equivalent amount with a solution of a peptide mixture for mass calibration (300 nmol/l Angiotensin II, 300 nmol/l Neurotensin, 150 nmol/l ACTHclip 18-39, 2.3 μmol/l bovine insulin B chain), and 1 μl of the obtained solution was spotted on a stainless probe and crystallized by spontaneously drying.

[0461] As measurement instruments, REFLEX MALDI-TOF mass spectrometer (manufactured by Bruker) and an N2 laser (337 nm) were used in combination.

[0462] The analysis by PMF (peptide-mass finger printing) was carried out using integration spectra data obtained by measuring 30 times at an accelerated voltage of 19.0 kV and a detector voltage of 1.50 kV under reflector mode conditions. Mass calibration was carried out by the internal standard method.

[0463] The PSD (post-source decay) analysis was carried out using integration spectra obtained by successively altering the reflection voltage and the detector voltage at an accelerated voltage of 27.5 kV.

[0464] The masses and amino acid sequences of the peptide fragments derived from the protein spot after digestion were thus determined.

(6) Identification of protein spot

[0465] From the amino acid sequence information of the digested peptide fragments derived from the protein spot obtained in the above (5), ORFs corresponding to the protein were searched on the genome sequence database of *Corynebacterium glutamicum* ATCC 13032 as constructed in Example 1 to identify the protein.

[0466] The identification of the protein was carried out using MS-Fit program and MS-Tag program of intranet protein prospector.

(a) Search and identification of gene encoding high-expression protein

[0467] In the proteins derived from *Corynebacterium glutamicum* ATCC 13032 showing high expression amounts in CBB-staining shown in Fig. 2A, the proteins corresponding to Spots-1, 2, 3, 4 and 5 were identified by the above method.

[0468] As a result, it was found that Spot-1 corresponded to enolase which was a protein having the amino acid sequence of SEQ ID NO:4585; Spot-2 corresponded to phosphoglycelate kinase which was a protein having the amino acid sequence of SEQ ID NO:5254; Spot-3 corresponded to glyceraldehyde-3-phosphate dehydrogenase which was

a protein having the amino acid sequence represented by SEQ ID NO:5255; Spot-4 corresponded to fructose bisphosphate aldolase which was a protein having the amino acid sequence represented by SEQ ID NO:6543; and Spot-5 corresponded to triose phosphate isomerase which was a protein having the amino acid sequence represented by SEQ ID NO:5252.

[0469] These genes, represented by SEQ ID NOS:1085, 1754, 1775, 3043 and 1752 encoding the proteins corresponding to Spots-1, 2, 3, 4 and 5, respectively, encoding the known proteins are important in the central metabolic pathway for maintaining the life of the microorganism. Particularly, it is suggested that the genes of Spots-2, 3 and 5 form an operon and a high-expression promoter is encoded in the upstream thereof (*J. of Eacteriol.*, *174*: 6067-6086 (1992)).

[0470] Also, the protein corresponding to Spot-9 in Fig. 2 was identified in the same manner as described above, and it was found that Spot-9 was an elongation factor Tu which was a protein having the amino acid sequence represented by SEQ ID No:6937, and that the protein was encoded by DNA having the nucleotide sequence represented by SEQ ID No:3437.

[0471] Based on these results, the proteins having high expression level were identified by proteome analysis using the genome sequence database of *Corynebacterium glutamicum* constructed in Example 1. Thus, the nucleotide sequences of the genes encoding the proteins and the nucleotide sequences upstream thereof could be searched simultaneously. Accordingly, it is shown that nucleotide sequences having a function as a high-expression promoter can be efficiently selected.

(b) Search and identification of modified protein

[0472] Among the proteins derived from *Corynebacterium glutamicum* FERM BP-7134 shown in Fig. 2B, Spots-6, 7 and 8 were identified by the above method. As a result, these three spots all corresponded to catalase which was a protein having the amino acid sequence represented by SEQ ID NO:3785.

[0473] Accordingly, all of Spots-6, 7 and 8 detected as spots differing in isoelectric mobility were all products derived from a catalase gene having the nucleotide sequence represented by SEQ ID No:285. Accordingly, it is shown that the catalase derived from *Corynebacterium glutamicum* FERM BP-7134 was modified after the translation.

[0474] Based on these results, it is confirmed that various modified proteins can be efficiently searched by proteome analysis using the genome sequence database of *Corynebacterium glutamicum* constructed in Example 1.

(c) Search and identification of expressed protein effective in lysine production

[0475] It was found out that in Fig. 2A (ATCC 13032: wild type strain), Fig. 2B (FERM BP-7134: lysine-producing strain) and Fig. 2C (FERM BP-158: lysine-highly producing strain), the catalase corresponding to Spot-8 and the elongation factor Tu corresponding to Spot-9 as identified above showed the higher expression level with an increase in the lysine productivity.

[0476] Based on these results, it was found that hopeful mutated proteins can be efficiently searched and identified in breeding aiming at strengthening the productivity of a target product by the proteome analysis using the genome sequence database of *Corynebacterium glutamicum* constructed in Example 1.

[0477] Moreover, useful mutation points of useful mutants can be easily specified by searching the nucleotide sequences (nucleotide sequences of promoter, ORF, or the like) relating to the identified proteins using the above database and using primers designed on the basis of the sequences. As a result of the fact that the mutation points are specified, industrially useful mutants which have the useful mutations or other useful mutations derived therefrom can be easily bred.

[0478] While the invention has been described in detail and with reference to specific embodiments thereof, it will be apparent to one of skill in the art that various changes and modifications can be made therein without departing from the spirit and scope thereof. All references cited herein are incorporated in their entirety.

Claims

1. A method for at least one of the following:

(A) identifying a mutation point of a gene derived from a mutant of a coryneform bacterium,
(B) measuring an expression amount of a gene derived from a coryneform bacterium,
(C) analyzing an expression profile of a gene derived from a coryneform bacterium,
(D) analyzing expression patterns of genes derived from a coryneform bacterium, or
(E) identifying a gene homologous to a gene derived from a coryneform bacterium,

said method comprising:

(a) producing a polynucleotide array by adhering to a solid support at least two polynucleotides selected from the group consisting of first polynucleotides comprising the nucleotide sequence represented by any one of SEQ ID NOS:1 to 3501, second polynucleotides which hybridize with the first polynucleotides under stringent conditions and third polynucleotides comprising a sequence of 10 to 200 continuous bases of the first or second polynucleotides.
(b) incubating the polynuclectide array with at least one of a labeled polynucleotide derived from a coryneform bacterium, a labeled polynucleotice derived from a mutant of the coryneform bacterium or a labeled polynucleotide to be examined, under hybridization conditions.
(c) detecting any hybridization, and
(d) analyzing the result of the hybridization.

2. The method according to claim 1, wherein the coryneform bacterium is a microorganism belonging to the genus *Corynebacterium*, the genus *Brevibacterium*, or the genus *Microbacterium*.

3. The method according to claim 2, wherein the microorganism belonging to the genus *Corynebacterium* is selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium callunae*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, and *Corynebacterium ammoniagenes*.

4. The method according to claim 1, wherein the polynucleotide derived from a coryneform bacterium, the polynucelotide derived from a mutant of the coryneform bacterium or the polynucleotide to be examined is a gene relating to the biosynthesis of at least one compound selected from an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid, and analogues thereof.

5. The method according to claim 1, wherein the polynucleotide to be examined is derived from *Escherichia coli*.

6. A polynucleotide array, comprising:

at least two polynucleotides selected from the group consisting of first polynucleotides comprising the nucleotide sequence represented by any one of SEQ ID NOS:1 to 3501, second polynucleotides which hybridize with the first polynucleotides under stringent conditions, and third polynucleotides comprising 10 to 200 continuous bases of the first or second polynucleotides, and
a solid support adhered thereto.

7. A polynucleotide comprising the nucleotide sequence represented by SEQ ID NO:1 or a polynucleotide having a homology of at least 80% with the polynucleotide.

8. A polynucleotide comprising any one of the nucleotide sequences represented by SEQ ID NOS:2 to 3431, or a polynucleotide which hybridizes with the polynucleotide under stringent conditions.

9. A polynucleotide encoding a polypeptide having any one of the amino acid sequences represented by SEQ ID NOS:3502 to 6931, or a polynucleotide which hybridizes therewith under stringent conditions.

10. A polynucleotide which is present in the 5' upstream or 3' downstream of a polynucleotide comprising the nucleotide sequence of any one of SEQ ID NOS:2 to 3431 in a whole polynucleotide comprising the nucleotide sequence represented by SEQ ID NO:1, and has an activity of regulating an expression of the polynucleotide.

11. A polynucleotide comprising 10 to 200 continuous bases in the nucleotide sequence of the polynucleotide of any one of claims 7 to 10, or a polynucleotide comprising a nucleotide sequence complementary to the polynucleotide comprising 10 to 200 continuous based.

12. A recombinant DNA comprising the polynucleotide of any one of claims 8 to 11.

13. A transformant comprising the polynucleotide of any one of claims 8 to 11 or the recombinant DNA of claim 12

14. A method for producing a polypeptide, comprising:

culturing the transformant of claim 13 in a medium to produce and accumulate a polypeptide encoded by the polynucleotide of claim 8 or 9 in the medium, and
recovering the polypeptide from the medium.

15. A method for producing at least one of an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid, and analogues thereof, comprising:

culturing the transformant of claim 13 in a medium to produce and accumulate at least one of an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid, and analogues thereof in the medium, and
recovering the at least one of the amino acid, the nucleic acid, the vitamin, the saccharide, the organic acid, and analogues thereof from the medium.

16. A polypeptide encoded by a polynucleotide comprising the nucleotide sequence selected from SEQ ID NOS:2 to 3431.

17. A polypeptide comprising the amino acid sequence selected from SEQ ID NOS:3502 to 6931.

18. The polypeptide according to claim 16 or 17, wherein at least one amino acid is deleted, replaced, inserted or added, said polypeptides having an activity which is substantially the same as that of the polypeptide without said at least one amino acid deletion, replacement, insertion or addition.

19. A polypeptide comprising an amino acid sequence having a homology of at least 60% with the amino acid sequence of the polypeptide of claim 16 or 17, and having an activity which is substantially the same as that of the polypeptide.

20. An antibody which recognizes the polypeptide of any one of claims 16 to 19.

21. A polypeptide array, comprising:

at least one polypeptide or partial fragment polypeptide selected from the polypeptides of claims 16 to 19 and partial fragment polypeptides of the polypeptides, and
a solid support adhered thereto.

22. A polypeptide array, comprising:

at least one antibody which recognizes a polypeptide or partial fragment polypeptide selected from the polypeptides of claims 16 to 19 and partial fragment polypeptides of the polypeptides, and
a solid support adhered thereto.

23. A system based on a computer for identifying a target sequence or a target structure motif derived from a coryneform bacterium, comprising the following:

(i) a user input device that inputs at least one nucleotide sequence information selected from SEQ ID NOS:1 to 3501, and target sequence or target structure motif information;
(ii) a data storage device for at least temporarily storing the input information;
(iii) a comparator that compares the at least one nucleotide sequence information selected from SEQ ID NOS: 1 to 3501 with the target sequence or target structure motif information, recorded by the data storage device for screening and analyzing nucleotide sequence information which is coincident with or analogous to the target sequence or target structure motif information; and
(iv) an output device that shows a screening or analyzing result obtained by the comparator.

24. A method based on a computer for identifying a target sequence or a target structure motif derived from a coryneform bacterium, comprising the following:

(i) inputting at least one nucleotide sequence information selected from SEQ ID NOS:1 to 3501, target sequence information or target structure motif information into a user input device;
(ii) at least temporarily storing said information;
(iii) comparing the at least one nucleotide sequence information selected from SEQ ID NOS:1 to 3501 with the target sequence or target structure motif information; and

(iv) screening and analyzing nucleotide sequence information which is coincident with or analogous to the target sequence or target structure motif information.

25. A system based on a computer for identifying a target sequence or a target structure motif derived from a coryneform bacterium, comprising the following:

(i) a user input device that inputs at least one amino acid sequence information selected from SEQ ID NOS: 3502 to 7001, and target sequence or target structure motif information;
(ii) a data storage device for at least temporarily storing the input information;
(iii) a comparator that compares the at least one amino acid sequence information selected from SEQ ID NOS: 3502 to 7001 with the target sequence or target structure motif information, recorded by the data storage device for screening and analyzing amino acid sequence information which is coincident with or analogous to the target sequence or target structure motif information; and
(iv) an output device that shows a screening or analyzing result obtained by the comparator.

26. A method based on a computer for identifying a target sequence or a target structure motif derived from a coryneform bacterium, comprising the following:

(i) inputting at least one amino acid sequence information selected from SEQ ID NOS:3502 to 7001, and target sequence information or target structure motif information into a user input device;
(ii) at least temporarily storing said information;
(iii) comparing the at least one amino acid sequence information selected from SEQ ID NOS 3502 to 7001 with the target sequence or target structure motif information; and
(iv) screening and analyzing amino acid sequence information which is coincident with or analogous to the target sequence or target structure motif information.

27. A system based on a computer for determining a function of a polypeptide encoded by a polynucleotide having a target nucleotide sequence derived from a coryneform bacterium, comprising the following:

(i) a user input device that inputs at least one nucleotide sequence information selected from SEQ ID NOS:2 to 3501, function information of a polypeptide encoded by the nucleotide sequence, and target nucleotide sequence information;
(ii) a data storage device for at least temporarily storing the input information;
(iii) a comparator that compares the at least one nucleotide sequence information selected from SEQ ID NOS: 2 to 3501 with the target nucleotide sequence information for determining a function of a polypeptide encoded by a polynucleotide having the target nucleotide sequence which is coincident with or analogous to the polynucleotide having at least one nucleotide sequence selected from SEQ ID NOS:2 to 3501; and
(iv) an output devices that shows a function obtained by the comparator.

28. A method based on a computer for determining a function of a polypeptide encoded by a polypeptide encoded by a polynucleotide having a target nucleotide sequence derived from a coryneform bacterium, comprising the following:

(i) inputting at least one nucleotide sequence information selected from SEQ ID NOS:2 to 3501, function information of a polypeptide encoded by the nucleotide sequence, and target nucleotide sequence information;
(ii) at least temporarily storing said information;
(iii) comparing the at least one nucleotide sequence information selected from SEQ ID NOS:2 to 3501 with the target nucleotide sequence information; and
(iv) determining a function of a polypeptide encoded by a polynucleotide having the target nucleotide sequence which is coincident with or analogous to the polynucleotide having at least one nucleotide sequence selected from SEQ ID NOS:2 to 3501.

29. A system based on a computer for determining a function of a polypeptide having a target amino acid sequence derived from a coryneform bacterium, comprising the following:

(i) a user input device that inputs at least one amino acid sequence information selected from SEQ ID NOS: 3502 to 7001, function information based on the amino acid sequence, and target amino acid sequence information;

(ii) a data storing device for at least temporarily storing the input information;
(iii) a comparator that compares the at least one amino acid sequence information selected from SEQ ID NOS: 3502 to 7001 with the target amino acid sequence information for determining a function of a polypeptide having the target amino acid sequence which is coincident with or analogous to the polypeptide having at least one amino acid sequence selected from SEQ ID NOS:3502 to 7001; and
(iv) an output device that shows a function obtained by the comparator.

30. A method based on a computer for determining a function of a polypeptide having a target amino acid sequence derived from a coryneform bacterium, comprising the following:

(i) inputting at least one amino acid sequence information selected from SEQ ID NOS:3502 to 7001, function information based on the amino acid sequence, and target amino acid sequence information;
(ii) at least temporarily storing said information;
(iii) comparing the at least one amino acid sequence information selected from SEQ ID NOS:3502 to 7001 with the target amino acid sequence information; and
(iv) determining a function of a polypeptide having the target amino acid sequence which is coincident with or analogous to the polypeptide having at least one amino acid sequence selected from SEQ ID NOS:3502 to 7001.

31. The system according to any one of claims 23, 25, 27 and 29, wherein a coryneform bacterium is a microorganism of the genus *Corynebacterium*, the genus *Brevibacterium*, or the genus *Microbacterium*.

32. The method according to any one of claims 24, 26, 28 and 30, wherein a coryneform bacterium is a microorganism of the genus *Corynebacterium*, the genus *Brevibacterium*, or the genus *Microbacterium*.

33. The system according to claim 31, wherein the microorganism belonging to the genus *Corynebacterium* is selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium callunae*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, and *Corynebacterium ammoniagenes*.

34. The method according to claim 32, wherein the microorganism belonging to the genus *Corynebacterium* is selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium callunae*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, and *Corynebacterium ammoniagenes*.

35. A recording medium or storage device which is readable by a computer in which at least one nucleotide sequence information selected from SEQ ID NOS:1 to 3501 or function information based on the nucleotide sequence is recorded, and is usable in the system of claim 23 or 27 or the method of claim 24 or 28.

36. A recording medium or storage device which is readable by a computer in which at least one amino acid sequence information selected from SEQ ID NOS:3502 to 7001 or function information based on the amino acid sequence is recorded, and is usable in the system of claim 25 or 29 or the method of claim 26 or 30.

37. The recording medium or storage device according to claim 35 or 36, which is a computer readable recording medium selected from the group consisting of a floppy disc, a hard disc, a magnetic tape, a random access memory (RAM), a read only memory (ROM), a magneto-optic disc (MO), CD-ROM, CD-R, CD-RW, DVD-ROM, DVD-RAM and DVD-RW.

38. A polypeptide having a homoserine dehydrogenase activity, comprising an amino acid sequence in which the Val residue at the 59th in the amino acid sequence of homoserine dehydrogenase derived from a coryneform bacterium is replaced with an amino acid residue other than a Val residue.

39. A polypeptide comprising an amino acid sequence in which the Val residue at the 59th position in the amino acid sequence as represented by SEQ ID NO:6952 is replaced with an amino acid residue other than a Val residue.

40. The polypeptide according to claim 38 or 39, wherein the Val residue at the 59th position is replaced with an Ala residue.

41. A polypeptide having pyruvate carboxylase activity comprising an amino acid sequence in which the Pro residue at the 458th position in the amino acid sequence of pyruvate carboxylase derived from a coryneform bacterium is replaced with an amino acid residue other than a Pro residue.

42. A polypeptide comprising an amino acid sequence in which the Pro residue at the 458th position in the amino acid sequence represented by SEQ ID NO:4265 is replaced with an amino acid residue other than a Pro residue.

43. The polypeptide according to claim 41 or 42, wherein the Pro residue at the 458th position is replaced with a Ser residue.

44. The polypeptide according to any one of claims 38 to 43, which is derived from *Corynebacterium glutamicum*.

45. A DNA encoding the polypeptide of any one of claims 38 to 44.

46. A recombinant DNA comprising the DNA of claim 45

47. A transformant comprising the recombinant DNA of claim 46.

48. A transformant comprising in its chromosome the DNA of claim 45.

49. The transformant according to claim 47 or 48, which is derived from a coryneform bacterium

50. The transformant according to claim 49, which is derived from *Corynebacterium glutamicum*.

51. A method for producing L-lysine, comprising:

culturing the transformant of any one of claims 47 to 50 in a medium to produce and accumulate L-lysine in the medium, and
recovering the L-lysine from the culture.

52. A method for breeding a coryneform bacterium using the nucleotide sequence information represented by SEQ ID NOS:1 to 3431, comprising the following:

(i) comparing a nucleotide sequence of a genome or gene of a production strain derived a coryneform bacterium which has been subjected to mutation breeding so as to produce at least one compound selected from an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid, and analogous thereof by a fermentation method, with a corresponding nucleotide sequence in SEQ ID NOS:1 to 3431;
(ii) identifying a mutation point present in the production strain based on a result obtained by (i);
(iii) introducing the mutation point into a coryneform bacterium which is free of the mutation point, or deleting the mutation point from a coryneform bacterium having the mutation point; and
(iv) examining productivity by the fermentation method of the compound selected in (i) of the coryneform bacterium obtained in (iii).

53. The method according to claim 52, wherein the gene is a gene encoding an enzyme in a biosynthetic pathway or a signal transmission pathway.

54. The method according to claim 52, wherein the mutation point is a mutation point relating to a useful mutation which improves or stabilizes the productivity.

55. A method for breading a coryneform bacterium using the nucleotide sequence information represented by SEQ ID NOS:1 to 3431, comprising:

(i) comparing a nucleotide sequence of a genome or gene of a production strain derived a coryneform bacterium which has been subjected to mutation breeding so as to produce at least one compound selected from an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid, and analogous thereof by a fermentation method, with a corresponding nucleotide sequence in SEQ ID NOS:1 to 3431;
(ii) identifying a mutation point present in the production strain based on a result obtain by (i);
(iii) deleting a mutation point from a coryneform bacterium having the mutation point; and

(iv) examining productivity by the fermentation method of the compound selected in (i) of the coryneform bacterium obtained in (iii).

56. The method according to claim 55, wherein the gene is a gene encoding an enzyme in a biosynthetic pathway or a signal transmission pathway.

57. The method according to claim 55, wherein the mutation point is a mutation point which decreases or destabilizes the productivity.

58. A method for breeding a coryneform bacterium using the nucleotide sequence information represented by SEQ ID NOS:2 to 3431, comprising the following:

(i) identifying an isozyme relating to biosynthesis of at least one compound selected from an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid, and analogous thereof, based on the nucleotide sequence information represented by SEQ ID NOS:2 to 3431;
(ii) classifying the isozyme identified in (i) into an isozyme having the same activity;
(iii) mutating all genes encoding the isozyme having the same activity simultaneously; and
(iv) examining productivity by a fermentation method of the compound selected in (i) of the coryneform bacterium which have been transformed with the gene obtained in (iii).

59. A method for breeding a coryneform bacterium using the nucleotide sequence information represented by SEQ ID NOS:2 to 3431, comprising the following:

(i) arranging a function information of an open reading frame (ORF) represented by SEQ ID NOS:2 to 3431;
(ii) allowing the arranged ORF to correspond to an enzyme on a known biosynthesis or signal transmission pathway;
(iii) explicating an unknown biosynthesis pathway or signal transmission pathway of a coryneform bacterium in combination with information relating known biosynthesis pathway or signal transmission pathway of a coryneform bacterium;
(iv) comparing the pathway explicated in (iii) with a biosynthesis pathway of a target useful product; and
(v) transgenetically varying a coryneform bacterium based on the nucleotide sequence information to either strengthen a pathway which is judged to be important in the biosynthesis of the target useful product in (iv) or weaken a pathway which is judged not to be important in the biosynthesis of the target useful product in (iv).

60. A coryneform bacterium, bred by the method of any one of claims 52 to 59.

61. The coryneform bacterium according to claim 60, which is a microorganism belonging to the genus *Corynebacterium*, the genus *Brevibacterium*, or the genus *Microbacterium*.

62. The coryneform bacterium according to claim 61, wherein the microorganism belonging to the genus *Corynebacterium* is selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium callunae*, *Corynebacterium herculis*, *corynebacterium lilium*, *Corynebacterium melassecola*, *Corynebacterium thermoamino genes*, and *Corynebacterium ammonia genes*.

63. A method for producing at least one compound selected from an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid and an analogue thereof, comprising:

culturing a coryneform bacterium of any one of claims 60 to 62 in a medium to produce and accumulate at least one compound selected from an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid, and analogues thereof;
recovering the compound from the culture.

64. The method according to claim 63, wherein the compound is L-lysine.

65. A method for identifying a protein relating to useful mutation based on proteome analysis, comprising the following:

(i) preparing

a protein derived from a bacterium of a production strain of a coryneform bacterium which has been subjected to mutation breeding by a fermentation process so as to produce at least one compound selected from an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid, and analogues thereof, and a protein derived from a bacterium of a parent strain of the production strain;

(ii) separating the proteins prepared in (i) by two dimensional electrophoresis;
(iii) detecting the separated proteins, and comparing an expression amount of the protein derived from the production strain with that derived from the parent strain;
(iv) treating the protein showing different expression amounts as a result of the comparison with a peptidase to extract peptide fragments;
(v) analyzing amino acid sequences of the peptide fragments obtained in (iv); and
(vi) comparing the amino acid sequences obtained in (v) with the amino acid sequence represented by SEQ ID NOS:3502 to 7001 to identifying the protein having the amino acid sequences.

66. The method according to claim 65, wherein the coryneform bacterium is a microorganism belonging to the genus *corynebacterium*, the genus *Brevibacterium*, or the genus *Microbacterium*.

67. The method according to claim 66, wherein the microorganism belonging to the genus *Corynebacterium* is selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium callunae*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, and *Corynebacterium ammoniagenes*.

68. A biologically pure culture of *Corynebacterium glutamicum* AHP-3 (FERM BP-7382).

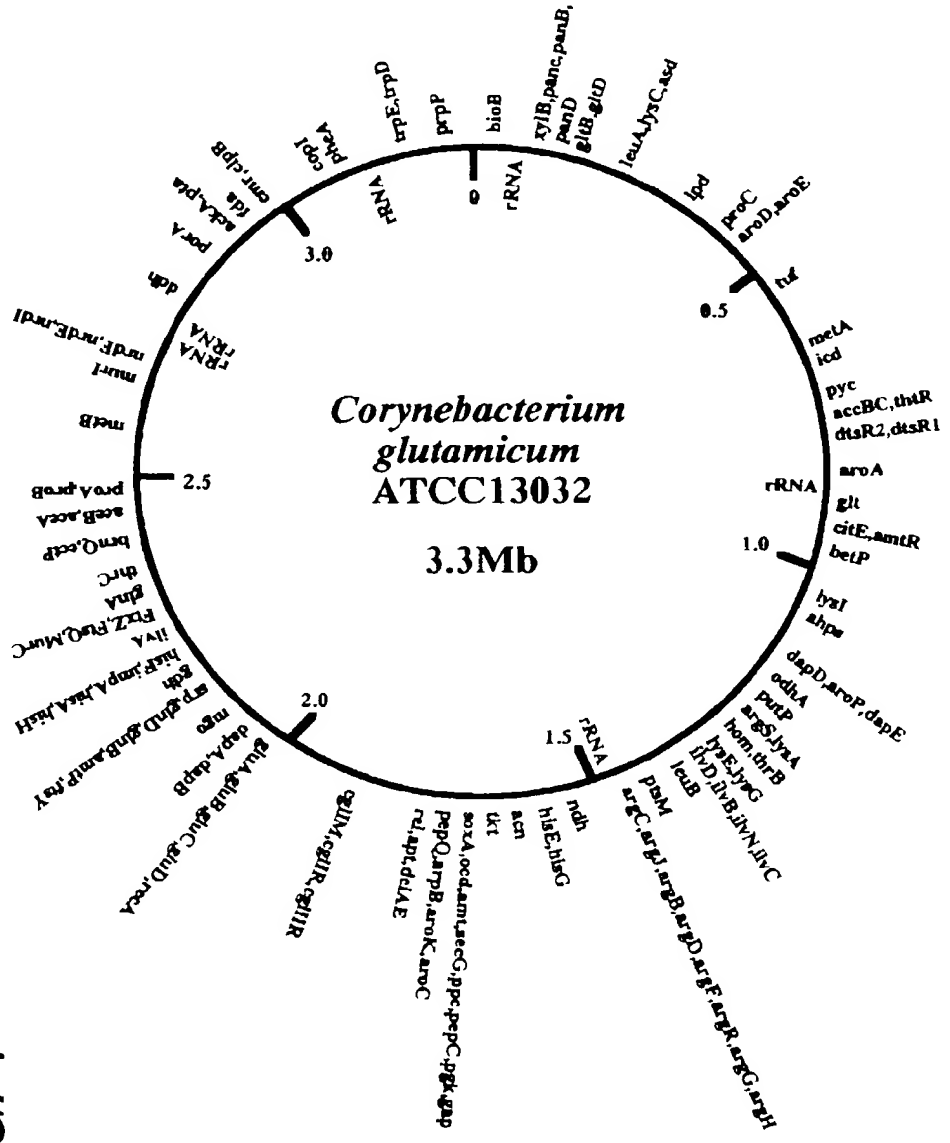


FIG. 1

FIG. 2A

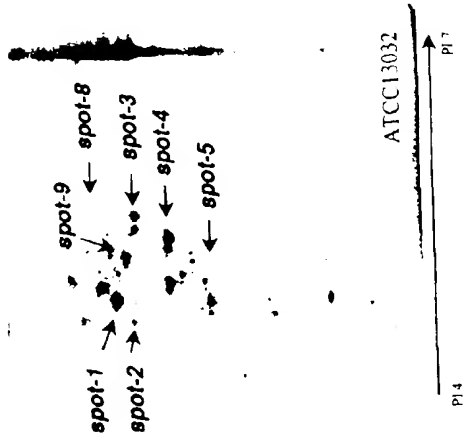


FIG. 2B

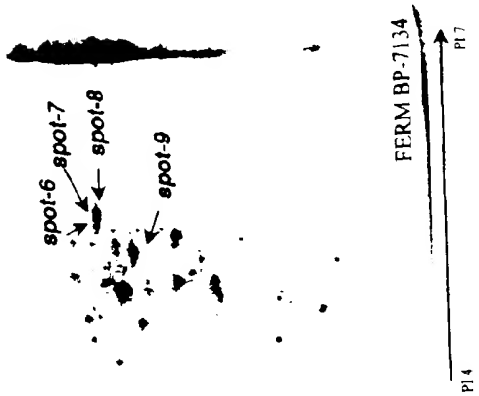


FIG. 2C

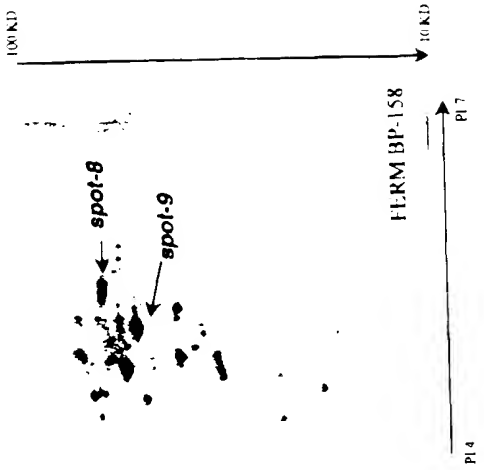


FIG. 3

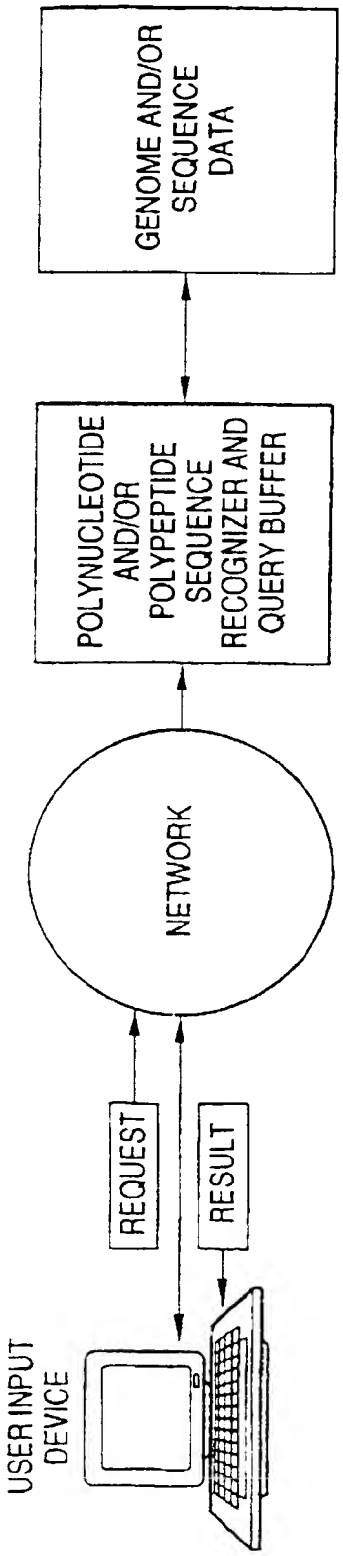
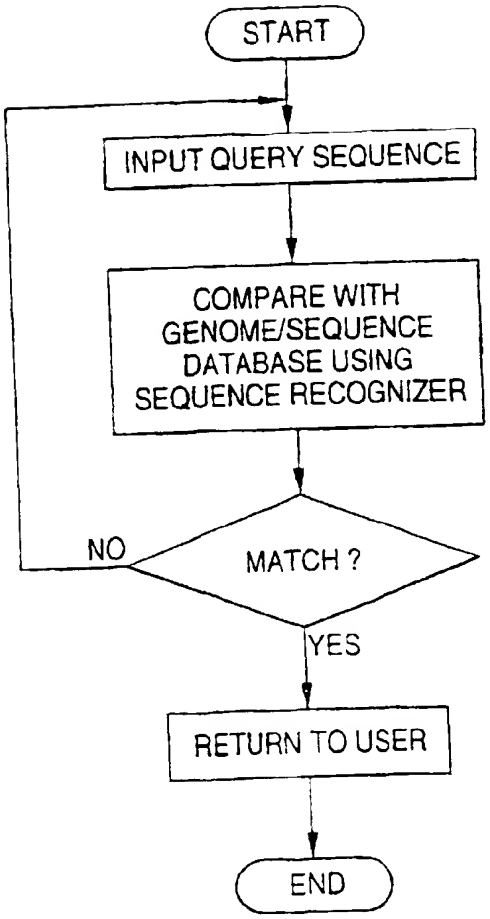


FIG. 4


START
INPUT QUERY SEQUENCE
COMPARE WITH GENOME/SEQUENCE DATABASE USING SEQUENCE RECOGNIZER
MATCH ?
NO
YES
RETURN TO USER
END